

Appendix



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CHAPTER 2: SUPPLEMENTARY INFORMATION

2.1. Increasing intergroup encounter detectability

In order to facilitate the detection of intergroup encounters by my team and to start the data collection of encounters as soon as possible, two methods were used:

Whatsapp group: I created a Whatsapp (Koum, Acto 2010) group which included all the people working for the MNP in the field at the time. This group was used to ask about the location of the habituated groups when we thought that we might be close to each other or getting closer and to estate encounters if neither I nor other observers of my team were around. Internet reception in Tangkoko was generally good and every person collecting data for the MNP had a smartphone in the field.

Alert system: When any person of my team detected an encounter for the first time, she would say “oh” three times loudly, in order to make aware to other team members that there was an intergroup encounter happening. Some member of the MNP used the system too. We developed this system since the MNP was already using 1 “Oh” to mean “Where are you?”, and 2 “ohs” to say “I am here”.

2.2. Calculation of location-based payoffs

2.2.1. BROWNIAN BRIDGE MOVEMENT MODELS: R SCRIPT

The original script for the calculation of BBMM was provided by James Waterman. I modified it in order to fit my data and the periods I required and eliminated parts I did not need.

Brownian Bridge Movement Models

#Make sure R (and R studio if used) are the last versions, to avoid problems loading the packages

1. Install and load required packages:

```
install.packages("raster")# To write the rasters and use them in QGIS
install.packages("rgdal")#write the calculated contours of the home ranges into vectors
install.packages("maptools")
install.packages("BBMM")
```

```
library(raster)
library(rgdal)
library(maptools)
library(BBMM)
```

2. Import GPS data and check:

#Remember to change "\" to "/" of the wd to avoid problems

```
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/BBMM/Project_BBMMs")
getwd()
dir()
gps.bbmm<-read.csv( "bbmmdata_igip.csv")
head(gps.bbmm)
str(gps.bbmm)
class(gps.bbmm)
```

3. Turn dataset into a SpatialPointsDataFrame (SPDF) by specifying that the "x" and "y" columns are the coordinates:

```
coordinates(gps.bbmm) <- c("x","y")
head(coordinates(gps.bbmm))
```

4. Check conversion to SPDF:

```
class(gps.bbmm)
```

5. Plot all gps points:

```
plot(gps.bbmm)
```

6. Plot each group with a different colour (random colours):

```
plot(gps.bbmm, col=gps.bbmm$group, pch=19, cex=0.6)
```

7. Plot each group with a different colour (specified colours):

```
col.list <- c("green", "red", "yellow")
palette(col.list)
plot(gps.bbmm, col=gps.bbmm$group, pch=21, cex=0.6)
```

8. Display current Coordinate Reference System (CRS) info:

```
proj4string(gps.bbmm)
```

9. Tell R the current CRS of the SPDF: (Code 4326 is WGS84):

```
proj4string(gps.bbmm) <- CRS("+init=epsg:4326")
summary(gps.bbmm)
```

10. Transform SPDF to chosen CRS (WGS84 Pseudo Mercator (3857)):

```
gps.bbmm <- spTransform(gps.bbmm, CRS("+init=epsg:3857"))
```

11. Check new CRS: Note that coordinates will appear in metres not degrees. This is what we need to proceed:

```
summary(gps.bbmm)
```

Data should now be in correct format to proceed with BBMM

12. Subset data frame by group and month:

##12.1 PB1

##12.1.1 All PB1

```
gps.bbmm.pb1 <- gps.bbmm[gps.bbmm$group == "PB1",]
```

##12.1.1 PB1 by month

```
gps.bbmm.pb1.oct <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "10",]
gps.bbmm.pb1.nov <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "11",]
gps.bbmm.pb1.dec <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "12",]
gps.bbmm.pb1.jan <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "1",]
gps.bbmm.pb1.feb <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "2",]
gps.bbmm.pb1.mar <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "3",]
gps.bbmm.pb1.apr <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "4",]
gps.bbmm.pb1.may <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "5",]
gps.bbmm.pb1.jun <- gps.bbmm.pb1[gps.bbmm.pb1$Month == "6",]
```

#12.2 R1

##12.2.1 All R1


```
gps.bbmm.r1 <- gps.bbmm[gps.bbmm$group == "R1",]
```

```
##12.2.1 R1 by month
```

```
gps.bbmm.r1.oct<- gps.bbmm.r1[gps.bbmm.r1$Month == "10",]  
gps.bbmm.r1.nov<- gps.bbmm.r1[gps.bbmm.r1$Month == "11",]  
gps.bbmm.r1.dec<- gps.bbmm.r1[gps.bbmm.r1$Month == "12",]  
gps.bbmm.r1.jan<- gps.bbmm.r1[gps.bbmm.r1$Month == "1",]  
gps.bbmm.r1.feb<- gps.bbmm.r1[gps.bbmm.r1$Month == "2",]  
gps.bbmm.r1.mar<- gps.bbmm.r1[gps.bbmm.r1$Month == "3",]  
gps.bbmm.r1.apr<- gps.bbmm.r1[gps.bbmm.r1$Month == "4",]  
gps.bbmm.r1.may<- gps.bbmm.r1[gps.bbmm.r1$Month == "5",]  
gps.bbmm.r1.jun<- gps.bbmm.r1[gps.bbmm.r1$Month == "6",]
```

```
#12.2 R2
```

```
##12.2.1 All R2
```

```
gps.bbmm.r2 <- gps.bbmm[gps.bbmm$group == "R2",]
```

```
##12.2.1 R1 by month
```

```
gps.bbmm.r2.oct<- gps.bbmm.r2[gps.bbmm.r2$Month == "10",]  
gps.bbmm.r2.nov<- gps.bbmm.r2[gps.bbmm.r2$Month == "11",]  
gps.bbmm.r2.dec<- gps.bbmm.r2[gps.bbmm.r2$Month == "12",]  
gps.bbmm.r2.jan<- gps.bbmm.r2[gps.bbmm.r2$Month == "1",]  
gps.bbmm.r2.feb<- gps.bbmm.r2[gps.bbmm.r2$Month == "2",]  
gps.bbmm.r2.mar<- gps.bbmm.r2[gps.bbmm.r2$Month == "3",]  
gps.bbmm.r2.apr<- gps.bbmm.r2[gps.bbmm.r2$Month == "4",]  
gps.bbmm.r2.may<- gps.bbmm.r2[gps.bbmm.r2$Month == "5",]  
gps.bbmm.r2.jun<- gps.bbmm.r2[gps.bbmm.r2$Month == "6",]
```

```
#13 BBMMs Calculations
```

```
##13.1 Create General PB1 group BBMM:
```

```
#Location error is 15
```

```
#cell.size is 190
```

```
#max.lag 15
```

```
##13.2 Annual PB1 BBMMs
```

```
bbmm.pb1<- brownian.bridge(x=gps.bbmm.pb1$x, y=gps.bbmm.pb1$y,  
                           time.lag=gps.bbmm.pb1$lag[-1], location.error=15,  
                           cell.size=190, max.lag=15)
```

```
##13.3 Monthly PB1 BBMMs
```

```
#The warning messages tell us that in the process of searching for the minimum, our function encountered an  
#illegal value causing it to return a value of missing.
```

```
#11 Warning messages in Oct and in Apr
```

```
bbmm.pb1.oct <- brownian.bridge(x=gps.bbmm.pb1.oct$x, y=gps.bbmm.pb1.oct$y,
                                time.lag=gps.bbmm.pb1.oct$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.nov <- brownian.bridge(x=gps.bbmm.pb1.nov$x, y=gps.bbmm.pb1.nov$y,
                                time.lag=gps.bbmm.pb1.nov$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.dec <- brownian.bridge(x=gps.bbmm.pb1.dec$x, y=gps.bbmm.pb1.dec$y,
                                time.lag=gps.bbmm.pb1.dec$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.jan <- brownian.bridge(x=gps.bbmm.pb1.jan$x, y=gps.bbmm.pb1.jan$y,
                                time.lag=gps.bbmm.pb1.jan$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.feb <- brownian.bridge(x=gps.bbmm.pb1.feb$x, y=gps.bbmm.pb1.feb$y,
                                time.lag=gps.bbmm.pb1.feb$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.mar <- brownian.bridge(x=gps.bbmm.pb1.mar$x, y=gps.bbmm.pb1.mar$y,
                                time.lag=gps.bbmm.pb1.mar$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.apr <- brownian.bridge(x=gps.bbmm.pb1.apr$x, y=gps.bbmm.pb1.apr$y,
                                time.lag=gps.bbmm.pb1.apr$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.may <- brownian.bridge(x=gps.bbmm.pb1.may$x, y=gps.bbmm.pb1.may$y,
                                time.lag=gps.bbmm.pb1.may$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
bbmm.pb1.jun <- brownian.bridge(x=gps.bbmm.pb1.jun$x, y=gps.bbmm.pb1.jun$y,
                                time.lag=gps.bbmm.pb1.jun$lag[-1], location.error=15,
                                cell.size=190, max.lag=15)
```

13.4 View summary of PB1 models:

```
bbmm.summary(bbmm.pb1)
```

```
bbmm.summary(bbmm.pb1.oct)
bbmm.summary(bbmm.pb1.nov)
bbmm.summary(bbmm.pb1.dec)
bbmm.summary(bbmm.pb1.jan)
bbmm.summary(bbmm.pb1.feb)
bbmm.summary(bbmm.pb1.mar)
bbmm.summary(bbmm.pb1.apr)
bbmm.summary(bbmm.pb1.may)
bbmm.summary(bbmm.pb1.jun)
```

13.3 Create (and plot) PB1 group BBMM homerange contours (choose % utilisation - 50,60,70,80,90,95):

#Annual

```
bbmm.contours.pb15095 = bbmm.contour(bbmm.pb1, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb195 = bbmm.contour(bbmm.pb1, levels=c(95), plot=TRUE)
bbmm.contours.pb150 = bbmm.contour(bbmm.pb1, levels=c(50), plot=TRUE)
```

#Monthly

```

bbmm.contours.pb1.oct5095 = bbmm.contour(bbmm.pb1.oct, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.oct95 = bbmm.contour(bbmm.pb1.oct, levels=c(95), plot=TRUE)

bbmm.contours.pb1.nov5095 = bbmm.contour(bbmm.pb1.nov, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.nov95 = bbmm.contour(bbmm.pb1.nov, levels=c(95), plot=TRUE)

bbmm.contours.pb1.dec5095 = bbmm.contour(bbmm.pb1.dec, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.dec95 = bbmm.contour(bbmm.pb1.dec, levels=c(95), plot=TRUE)

bbmm.contours.pb1.jan5095 = bbmm.contour(bbmm.pb1.jan, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.jan95 = bbmm.contour(bbmm.pb1.jan, levels=c(95), plot=TRUE)

bbmm.contours.pb1.feb5095 = bbmm.contour(bbmm.pb1.feb, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.feb95 = bbmm.contour(bbmm.pb1.feb, levels=c(95), plot=TRUE)

bbmm.contours.pb1.mar5095 = bbmm.contour(bbmm.pb1.mar, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.mar95 = bbmm.contour(bbmm.pb1.mar, levels=c(95), plot=TRUE)

bbmm.contours.pb1.apr5095 = bbmm.contour(bbmm.pb1.apr, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.apr95 = bbmm.contour(bbmm.pb1.apr, levels=c(95), plot=TRUE)

bbmm.contours.pb1.may5095 = bbmm.contour(bbmm.pb1.may, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.may95 = bbmm.contour(bbmm.pb1.may, levels=c(95), plot=TRUE)

bbmm.contours.pb1.jun5095 = bbmm.contour(bbmm.pb1.jun, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.pb1.jun95 = bbmm.contour(bbmm.pb1.jun, levels=c(95), plot=TRUE)

```

14.1 Create R1 group BBMMs:

```

#Annual
bbmm.r1 <- brownian.bridge(x=gps.bbmm.r1$x, y=gps.bbmm.r1$y,
                           time.lag=gps.bbmm.r1$lag[-1], location.error=15,
                           cell.size=190, max.lag=15)

#Monthly
bbmm.r1.oct <- brownian.bridge(x=gps.bbmm.r1.oct$x, y=gps.bbmm.r1.oct$y,
                               time.lag=gps.bbmm.r1.oct$lag[-1], location.error=15,
                               cell.size=190, max.lag=15)
bbmm.r1.nov <- brownian.bridge(x=gps.bbmm.r1.nov$x, y=gps.bbmm.r1.nov$y,
                               time.lag=gps.bbmm.r1.nov$lag[-1], location.error=15,
                               cell.size=190, max.lag=15)
bbmm.r1.dec <- brownian.bridge(x=gps.bbmm.r1.dec$x, y=gps.bbmm.r1.dec$y,
                               time.lag=gps.bbmm.r1.dec$lag[-1], location.error=15,
                               cell.size=190, max.lag=15)
bbmm.r1.jan <- brownian.bridge(x=gps.bbmm.r1.jan$x, y=gps.bbmm.r1.jan$y,
                               time.lag=gps.bbmm.r1.jan$lag[-1], location.error=15,
                               cell.size=190, max.lag=15)
bbmm.r1.feb <- brownian.bridge(x=gps.bbmm.r1.feb$x, y=gps.bbmm.r1.feb$y,
                               time.lag=gps.bbmm.r1.feb$lag[-1], location.error=15,
                               cell.size=190, max.lag=15)
bbmm.r1.mar <- brownian.bridge(x=gps.bbmm.r1.mar$x, y=gps.bbmm.r1.mar$y,
                               time.lag=gps.bbmm.r1.mar$lag[-1], location.error=15,
                               cell.size=190, max.lag=15)
bbmm.r1.apr <- brownian.bridge(x=gps.bbmm.r1.apr$x, y=gps.bbmm.r1.apr$y,
                               time.lag=gps.bbmm.r1.apr$lag[-1], location.error=15,

```

```
cell.size=190, max.lag=15)
bbmm.r1.may <- brownian.bridge(x=gps.bbmm.r1.may$x, y=gps.bbmm.r1.may$y,
                             time.lag=gps.bbmm.r1.may$lag[-1], location.error=15,
                             cell.size=190, max.lag=15)
bbmm.r1.jun <- brownian.bridge(x=gps.bbmm.r1.jun$x, y=gps.bbmm.r1.jun$y,
                             time.lag=gps.bbmm.r1.jun$lag[-1], location.error=15,
                             cell.size=190, max.lag=15)
```

14.2 View summary of R1 model:

```
#Annual
bbmm.summary(bbmm.r1)

#Monthly
bbmm.summary(bbmm.r1.oct)
bbmm.summary(bbmm.r1.nov)
bbmm.summary(bbmm.r1.dec)
bbmm.summary(bbmm.r1.jan)
bbmm.summary(bbmm.r1.feb)
bbmm.summary(bbmm.r1.mar)
bbmm.summary(bbmm.r1.apr)
bbmm.summary(bbmm.r1.may)
bbmm.summary(bbmm.r1.jun)
```

14.3 Create (and plot) R1 group BBMM homerange contours (choose % utilisation - 50,60,70,80,90,95):

```
#Annual
bbmm.contours.r15095 = bbmm.contour(bbmm.r1, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r195 = bbmm.contour(bbmm.r1, levels=c(95), plot=TRUE)
bbmm.contours.r150 = bbmm.contour(bbmm.r1, levels=c(50), plot=TRUE)

#Monthly
bbmm.contours.r1.oct5095 = bbmm.contour(bbmm.r1.oct, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.oct95 = bbmm.contour(bbmm.r1.oct, levels=c(95), plot=TRUE)

bbmm.contours.r1.nov5095 = bbmm.contour(bbmm.r1.nov, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.nov95 = bbmm.contour(bbmm.r1.nov, levels=c(95), plot=TRUE)

bbmm.contours.r1.dec5095 = bbmm.contour(bbmm.r1.dec, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.dec95 = bbmm.contour(bbmm.r1.dec, levels=c(95), plot=TRUE)

bbmm.contours.r1.jan5095 = bbmm.contour(bbmm.r1.jan, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.jan95 = bbmm.contour(bbmm.r1.jan, levels=c(95), plot=TRUE)

bbmm.contours.r1.feb5095 = bbmm.contour(bbmm.r1.feb, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.feb95 = bbmm.contour(bbmm.r1.feb, levels=c(95), plot=TRUE)

bbmm.contours.r1.mar5095 = bbmm.contour(bbmm.r1.mar, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.mar95 = bbmm.contour(bbmm.r1.mar, levels=c(95), plot=TRUE)

bbmm.contours.r1.apr5095 = bbmm.contour(bbmm.r1.apr, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.apr95 = bbmm.contour(bbmm.r1.apr, levels=c(95), plot=TRUE)

bbmm.contours.r1.may5095 = bbmm.contour(bbmm.r1.may, levels=c(50,60,70,80,90,95), plot=TRUE)
```

```
bbmm.contours.r1.may95 = bbmm.contour(bbmm.r1.may, levels=c(95), plot=TRUE)

bbmm.contours.r1.jun5095 = bbmm.contour(bbmm.r1.jun, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r1.jun95 = bbmm.contour(bbmm.r1.jun, levels=c(95), plot=TRUE)

### 15.1 Create R2 group BBMM:
#Annual
bbmm.r2<- brownian.bridge(x=gps.bbmm.r2$x, y=gps.bbmm.r2$y,
                          time.lag=gps.bbmm.r2$lag[-1], location.error=15,
                          cell.size=190, max.lag=15)

#Monthly
bbmm.r2.oct <- brownian.bridge(x=gps.bbmm.r2.oct$x, y=gps.bbmm.r2.oct$y,
                              time.lag=gps.bbmm.r2.oct$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.nov <- brownian.bridge(x=gps.bbmm.r2.nov$x, y=gps.bbmm.r2.nov$y,
                              time.lag=gps.bbmm.r2.nov$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.dec <- brownian.bridge(x=gps.bbmm.r2.dec$x, y=gps.bbmm.r2.dec$y,
                              time.lag=gps.bbmm.r2.dec$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.jan <- brownian.bridge(x=gps.bbmm.r2.jan$x, y=gps.bbmm.r2.jan$y,
                              time.lag=gps.bbmm.r2.jan$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.feb <- brownian.bridge(x=gps.bbmm.r2.feb$x, y=gps.bbmm.r2.feb$y,
                              time.lag=gps.bbmm.r2.feb$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.mar <- brownian.bridge(x=gps.bbmm.r2.mar$x, y=gps.bbmm.r2.mar$y,
                              time.lag=gps.bbmm.r2.mar$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.apr <- brownian.bridge(x=gps.bbmm.r2.apr$x, y=gps.bbmm.r2.apr$y,
                              time.lag=gps.bbmm.r2.apr$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.may <- brownian.bridge(x=gps.bbmm.r2.may$x, y=gps.bbmm.r2.may$y,
                              time.lag=gps.bbmm.r2.may$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)
bbmm.r2.jun <- brownian.bridge(x=gps.bbmm.r2.jun$x, y=gps.bbmm.r2.jun$y,
                              time.lag=gps.bbmm.r2.jun$lag[-1], location.error=15,
                              cell.size=190, max.lag=15)

# 15.2 View summary of R2 model:
#Annual
bbmm.summary(bbmm.r2)

#Monthly
bbmm.summary(bbmm.r2.oct)
bbmm.summary(bbmm.r2.nov)
bbmm.summary(bbmm.r2.dec)
bbmm.summary(bbmm.r2.jan)
bbmm.summary(bbmm.r2.feb)
bbmm.summary(bbmm.r2.mar)
bbmm.summary(bbmm.r2.apr)
bbmm.summary(bbmm.r2.may)
bbmm.summary(bbmm.r2.jun)

# 15.3 Create (and plot) R2 group BBMM homerange contours (choose % utilisation - 50,60,70,80,90,95):
# Annual
```

```
bbmm.contours.r25095 = bbmm.contour(bbmm.r2, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r295 = bbmm.contour(bbmm.r2, levels=c(95), plot=TRUE)
bbmm.contours.r250 = bbmm.contour(bbmm.r2, levels=c(50), plot=TRUE)

#Monthly
bbmm.contours.r2.oct5095 = bbmm.contour(bbmm.r2.oct, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.oct95 = bbmm.contour(bbmm.r2.oct, levels=c(95), plot=TRUE)

bbmm.contours.r2.nov5095 = bbmm.contour(bbmm.r2.nov, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.nov95 = bbmm.contour(bbmm.r2.nov, levels=c(95), plot=TRUE)

bbmm.contours.r2.dec5095 = bbmm.contour(bbmm.r2.dec, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.dec95 = bbmm.contour(bbmm.r2.dec, levels=c(95), plot=TRUE)

bbmm.contours.r2.jan5095 = bbmm.contour(bbmm.r2.jan, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.jan95 = bbmm.contour(bbmm.r2.jan, levels=c(95), plot=TRUE)

bbmm.contours.r2.feb5095 = bbmm.contour(bbmm.r2.feb, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.feb95 = bbmm.contour(bbmm.r2.feb, levels=c(95), plot=TRUE)

bbmm.contours.r2.mar5095 = bbmm.contour(bbmm.r2.mar, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.mar95 = bbmm.contour(bbmm.r2.mar, levels=c(95), plot=TRUE)

bbmm.contours.r2.apr5095 = bbmm.contour(bbmm.r2.apr, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.apr95 = bbmm.contour(bbmm.r2.apr, levels=c(95), plot=TRUE)

bbmm.contours.r2.may5095 = bbmm.contour(bbmm.r2.may, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.may95 = bbmm.contour(bbmm.r2.may, levels=c(95), plot=TRUE)

bbmm.contours.r2.jun5095 = bbmm.contour(bbmm.r2.jun, levels=c(50,60,70,80,90,95), plot=TRUE)
bbmm.contours.r2.jun95 = bbmm.contour(bbmm.r2.jun, levels=c(95), plot=TRUE)
```

18. Create contour shapefiles for output and visualisation in GIS:

```
# 18.1 Create PB1 raster and contour shapefiles:
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group
level/BBMM/Project_BBMMs/RastersAndVectors")
dir()

#Annual PB1
Annual_out.pb1<- data.frame(x=bbmm.pb1$x,y=bbmm.pb1$y,z=bbmm.pb1$probability)
Annual_out.pb1.raster <- rasterFromXYZ(Annual_out.pb1,crs=CRS("+init=epsg:3857"),digits=4)
plot(Annual_out.pb1.raster)
writeRaster(Annual_out.pb1.raster, 'Annual hr pb1 .tif')

pb1.raster.contour <- rasterToContour(Annual_out.pb1.raster,levels=bbmm.contours.pb15095$Z)
pb1.raster.contour <- spChFIDs(pb1.raster.contour,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour,dsn=".",layer="Annual BBMM (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95 <- rasterToContour(Annual_out.pb1.raster,levels=bbmm.contours.pb195$Z)
pb1.raster.contour95 <- spChFIDs(pb1.raster.contour95,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95,dsn=".",layer="Annual BBMM(pb195)",driver="ESRI Shapefile")

pb1.raster.contour50 <- rasterToContour(Annual_out.pb1.raster,levels=bbmm.contours.pb150$Z)
```

```
pb1.raster.contour50 <- spChFIDs(pb1.raster.contour50,paste(c(50),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour50,dsn=".",layer="Annual BBMM(pb150)",driver="ESRI Shapefile")

#OCT PB1
out.pb1.oct <- data.frame(x=bbmm.pb1.oct$x,y=bbmm.pb1.oct$y,z=bbmm.pb1.oct$probability)
out.pb1.raster.oct <- rasterFromXYZ(out.pb1.oct,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.oct)
writeRaster(out.pb1.raster.oct, 'pb1 BBMMoct.tif')

pb1.raster.contour.oct <- rasterToContour(out.pb1.raster.oct,levels=bbmm.contours.pb1.oct5095$Z)
pb1.raster.contour.oct <- spChFIDs(pb1.raster.contour.oct,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour.oct,dsn=".",layer="BBMMoct (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.oct <- rasterToContour(out.pb1.raster.oct,levels=bbmm.contours.pb1.oct95$Z)
pb1.raster.contour95.oct <- spChFIDs(pb1.raster.contour95.oct,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.oct,dsn=".",layer="BBMMoct (pb195)",driver="ESRI Shapefile")

#NOV PB1
out.pb1.nov <- data.frame(x=bbmm.pb1.nov$x,y=bbmm.pb1.nov$y,z=bbmm.pb1.nov$probability)
out.pb1.raster.nov <- rasterFromXYZ(out.pb1.nov,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.nov)
writeRaster(out.pb1.raster.nov, 'pb1 BBMMnov.tif')

pb1.raster.contour.nov <- rasterToContour(out.pb1.raster.nov,levels=bbmm.contours.pb1.nov5095$Z)
pb1.raster.contour.nov <- spChFIDs(pb1.raster.contour.nov,paste(c(50,60,70,80,90,95),"% Contour
Line",sep=""))
writeOGR(obj=pb1.raster.contour.nov,dsn=".",layer="BBMMnov (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.nov <- rasterToContour(out.pb1.raster.nov,levels=bbmm.contours.pb1.nov95$Z)
pb1.raster.contour95.nov <- spChFIDs(pb1.raster.contour95.nov,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.nov,dsn=".",layer="BBMMnov (pb195)",driver="ESRI Shapefile")

#DEC PB1
out.pb1.dec <- data.frame(x=bbmm.pb1.dec$x,y=bbmm.pb1.dec$y,z=bbmm.pb1.dec$probability)
out.pb1.raster.dec <- rasterFromXYZ(out.pb1.dec,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.dec)
writeRaster(out.pb1.raster.dec, 'pb1 BBMMdec.tif')

pb1.raster.contour.dec <- rasterToContour(out.pb1.raster.dec,levels=bbmm.contours.pb1.dec5095$Z)
pb1.raster.contour.dec <- spChFIDs(pb1.raster.contour.dec,paste(c(50,60,70,80,90,95),"% Contour
Line",sep=""))
writeOGR(obj=pb1.raster.contour.dec,dsn=".",layer="BBMMdec (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.dec <- rasterToContour(out.pb1.raster.dec,levels=bbmm.contours.pb1.dec95$Z)
pb1.raster.contour95.dec <- spChFIDs(pb1.raster.contour95.dec,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.dec,dsn=".",layer="BBMMdec (pb195)",driver="ESRI Shapefile")

#JAN PB1
```

```

out.pb1.jan <- data.frame(x=bbmm.pb1.jan$x,y=bbmm.pb1.jan$y,z=bbmm.pb1.jan$probability)
out.pb1.raster.jan <- rasterFromXYZ(out.pb1.jan,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.jan)
writeRaster(out.pb1.raster.jan, 'pb1 BBMMjan.tif')

pb1.raster.contour.jan <- rasterToContour(out.pb1.raster.jan,levels=bbmm.contours.pb1.jan5095$Z)
pb1.raster.contour.jan <- spChFIDs(pb1.raster.contour.jan,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour.jan,dsn=".",layer="BBMMjan (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.jan <- rasterToContour(out.pb1.raster.jan,levels=bbmm.contours.pb1.jan95$Z)
pb1.raster.contour95.jan <- spChFIDs(pb1.raster.contour95.jan,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.jan,dsn=".",layer="BBMMjan (pb195)",driver="ESRI Shapefile")

#FEB PB1
out.pb1.feb <- data.frame(x=bbmm.pb1.feb$x,y=bbmm.pb1.feb$y,z=bbmm.pb1.feb$probability)
out.pb1.raster.feb <- rasterFromXYZ(out.pb1.feb,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.feb)
writeRaster(out.pb1.raster.feb, 'pb1 BBMMfeb.tif')

pb1.raster.contour.feb <- rasterToContour(out.pb1.raster.feb,levels=bbmm.contours.pb1.feb5095$Z)
pb1.raster.contour.feb <- spChFIDs(pb1.raster.contour.feb,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour.feb,dsn=".",layer="BBMMfeb (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.feb <- rasterToContour(out.pb1.raster.feb,levels=bbmm.contours.pb1.feb95$Z)
pb1.raster.contour95.feb <- spChFIDs(pb1.raster.contour95.feb,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.feb,dsn=".",layer="BBMMfeb (pb195)",driver="ESRI Shapefile")

#MAR PB1
out.pb1.mar <- data.frame(x=bbmm.pb1.mar$x,y=bbmm.pb1.mar$y,z=bbmm.pb1.mar$probability)
out.pb1.raster.mar <- rasterFromXYZ(out.pb1.mar,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.mar)
writeRaster(out.pb1.raster.mar, 'pb1 BBMMmar.tif')

pb1.raster.contour.mar <- rasterToContour(out.pb1.raster.mar,levels=bbmm.contours.pb1.mar5095$Z)
pb1.raster.contour.mar <- spChFIDs(pb1.raster.contour.mar,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour.mar,dsn=".",layer="BBMMmar (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.mar <- rasterToContour(out.pb1.raster.mar,levels=bbmm.contours.pb1.mar95$Z)
pb1.raster.contour95.mar <- spChFIDs(pb1.raster.contour95.mar,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.mar,dsn=".",layer="BBMMmar (pb195)",driver="ESRI Shapefile")

#APR PB1
out.pb1.apr <- data.frame(x=bbmm.pb1.apr$x,y=bbmm.pb1.apr$y,z=bbmm.pb1.apr$probability)
out.pb1.raster.apr <- rasterFromXYZ(out.pb1.apr,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.apr)
writeRaster(out.pb1.raster.apr, 'pb1 BBMMapr.tif')

pb1.raster.contour.apr <- rasterToContour(out.pb1.raster.apr,levels=bbmm.contours.pb1.apr5095$Z)
pb1.raster.contour.apr <- spChFIDs(pb1.raster.contour.apr,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour.apr,dsn=".",layer="BBMMapr (pb150-95)",driver="ESRI Shapefile")

```



```

pb1.raster.contour95.apr <- rasterToContour(out.pb1.raster.apr,levels=bbmm.contours.pb1.apr95$Z)
pb1.raster.contour95.apr <- spChFIDs(pb1.raster.contour95.apr,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.apr,dsn=".",layer="BBMMApr (pb195)",driver="ESRI Shapefile")

#MAY PB1
out.pb1.may <- data.frame(x=bbmm.pb1.may$x,y=bbmm.pb1.may$y,z=bbmm.pb1.may$probability)
out.pb1.raster.may <- rasterFromXYZ(out.pb1.may,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.may)
writeRaster(out.pb1.raster.may, 'pb1 BBMMmay.tif')

pb1.raster.contour.may <- rasterToContour(out.pb1.raster.may,levels=bbmm.contours.pb1.may5095$Z)
pb1.raster.contour.may <- spChFIDs(pb1.raster.contour.may,paste(c(50,60,70,80,90,95),"% Contour
Line",sep=""))
writeOGR(obj=pb1.raster.contour.may,dsn=".",layer="BBMMmay (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.may <- rasterToContour(out.pb1.raster.may,levels=bbmm.contours.pb1.may95$Z)
pb1.raster.contour95.may <- spChFIDs(pb1.raster.contour95.may,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.may,dsn=".",layer="BBMMmay (pb195)",driver="ESRI Shapefile")

#JUN PB1
out.pb1.jun <- data.frame(x=bbmm.pb1.jun$x,y=bbmm.pb1.jun$y,z=bbmm.pb1.jun$probability)
out.pb1.raster.jun <- rasterFromXYZ(out.pb1.jun,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.pb1.raster.jun)
writeRaster(out.pb1.raster.jun, 'pb1 BBMMjun.tif')

pb1.raster.contour.jun <- rasterToContour(out.pb1.raster.jun,levels=bbmm.contours.pb1.jun5095$Z)
pb1.raster.contour.jun <- spChFIDs(pb1.raster.contour.jun,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour.jun,dsn=".",layer="BBMMjun (pb150-95)",driver="ESRI Shapefile")

pb1.raster.contour95.jun <- rasterToContour(out.pb1.raster.jun,levels=bbmm.contours.pb1.jun95$Z)
pb1.raster.contour95.jun <- spChFIDs(pb1.raster.contour95.jun,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=pb1.raster.contour95.jun,dsn=".",layer="BBMMjun (pb195)",driver="ESRI Shapefile")

# 18.2 Create R1 raster and contour shapefiles:

#Annual r1
Annual_out.r1<- data.frame(x=bbmm.r1$x,y=bbmm.r1$y,z=bbmm.r1$probability)
Annual_out.r1.raster <- rasterFromXYZ(Annual_out.r1,crs=CRS("+init=epsg:3857"),digits=4)
plot(Annual_out.r1.raster)
writeRaster(Annual_out.r1.raster, 'Annual hr r1 .tif')

r1.raster.contour <- rasterToContour(Annual_out.r1.raster,levels=bbmm.contours.r15095$Z)
r1.raster.contour <- spChFIDs(r1.raster.contour,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour,dsn=".",layer="Annual BBMM (r150-95)",driver="ESRI Shapefile")

r1.raster.contour95 <- rasterToContour(Annual_out.r1.raster,levels=bbmm.contours.r195$Z)
r1.raster.contour95 <- spChFIDs(r1.raster.contour95,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95,dsn=".",layer="Annual BBMM(r195)",driver="ESRI Shapefile")

r1.raster.contour50 <- rasterToContour(Annual_out.r1.raster,levels=bbmm.contours.r150$Z)
r1.raster.contour50 <- spChFIDs(r1.raster.contour50,paste(c(50),"% Contour Line",sep=""))

```

```
writeOGR(obj=r1.raster.contour50,dsn=".",layer="Annual BBMM(r150)",driver="ESRI Shapefile")

#OCT r1
out.r1.oct <- data.frame(x=bbmm.r1.oct$x,y=bbmm.r1.oct$y,z=bbmm.r1.oct$probability)
out.r1.raster.oct <- rasterFromXYZ(out.r1.oct,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.oct)
writeRaster(out.r1.raster.oct, 'r1 BBMMoct.tif')

r1.raster.contour.oct <- rasterToContour(out.r1.raster.oct,levels=bbmm.contours.r1.oct5095$Z)
r1.raster.contour.oct <- spChFIDs(r1.raster.contour.oct,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.oct,dsn=".",layer="BBMMoct (r150-95)",driver="ESRI Shapefile")

r1.raster.contour95.oct <- rasterToContour(out.r1.raster.oct,levels=bbmm.contours.r1.oct95$Z)
r1.raster.contour95.oct <- spChFIDs(r1.raster.contour95.oct,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.oct,dsn=".",layer="BBMMoct (r195)",driver="ESRI Shapefile")

#NOV r1
out.r1.nov <- data.frame(x=bbmm.r1.nov$x,y=bbmm.r1.nov$y,z=bbmm.r1.nov$probability)
out.r1.raster.nov <- rasterFromXYZ(out.r1.nov,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.nov)
writeRaster(out.r1.raster.nov, 'r1 BBMMnov.tif')

r1.raster.contour.nov <- rasterToContour(out.r1.raster.nov,levels=bbmm.contours.r1.nov5095$Z)
r1.raster.contour.nov <- spChFIDs(r1.raster.contour.nov,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.nov,dsn=".",layer="BBMMnov (r150-95)",driver="ESRI Shapefile")

r1.raster.contour95.nov <- rasterToContour(out.r1.raster.nov,levels=bbmm.contours.r1.nov95$Z)
r1.raster.contour95.nov <- spChFIDs(r1.raster.contour95.nov,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.nov,dsn=".",layer="BBMMnov (r195)",driver="ESRI Shapefile")

#DEC r1
out.r1.dec <- data.frame(x=bbmm.r1.dec$x,y=bbmm.r1.dec$y,z=bbmm.r1.dec$probability)
out.r1.raster.dec <- rasterFromXYZ(out.r1.dec,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.dec)
writeRaster(out.r1.raster.dec, 'r1 BBMMdec.tif')

r1.raster.contour.dec <- rasterToContour(out.r1.raster.dec,levels=bbmm.contours.r1.dec5095$Z)
r1.raster.contour.dec <- spChFIDs(r1.raster.contour.dec,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.dec,dsn=".",layer="BBMMdec (r150-95)",driver="ESRI Shapefile")

r1.raster.contour95.dec <- rasterToContour(out.r1.raster.dec,levels=bbmm.contours.r1.dec95$Z)
r1.raster.contour95.dec <- spChFIDs(r1.raster.contour95.dec,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.dec,dsn=".",layer="BBMMdec (r195)",driver="ESRI Shapefile")

#JAN R1
out.r1.jan <- data.frame(x=bbmm.r1.jan$x,y=bbmm.r1.jan$y,z=bbmm.r1.jan$probability)
out.r1.raster.jan <- rasterFromXYZ(out.r1.jan,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.jan)
writeRaster(out.r1.raster.jan, 'r1 BBMMjan.tif')

r1.raster.contour.jan <- rasterToContour(out.r1.raster.jan,levels=bbmm.contours.r1.jan5095$Z)
```

```

r1.raster.contour.jan <- spChFIDs(r1.raster.contour.jan,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.jan,dsn=".",layer="BBMMjan (r150-95)",driver="ESRI Shapefile")
#Note that with this given cell.size the layer of 90% and 95% are the same for jan r1, there are only 5 contours
created, while normally should be 6 contours
bbmm.contours.r1.jan5095 #Here is possibl to see that 90% and 95% have the same UD% and thus same value
and layer
r1.raster.contour95.jan <- rasterToContour(out.r1.raster.jan,levels=bbmm.contours.r1.jan95$Z)
r1.raster.contour95.jan <- spChFIDs(r1.raster.contour95.jan,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.jan,dsn=".",layer="BBMMjan (r195)",driver="ESRI Shapefile")

```

#FEB R1

```

out.r1.feb <- data.frame(x=bbmm.r1.feb$x,y=bbmm.r1.feb$y,z=bbmm.r1.feb$probability)
out.r1.raster.feb <- rasterFromXYZ(out.r1.feb,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.feb)
writeRaster(out.r1.raster.feb, 'r1 BBMMfeb.tif')

```

```

r1.raster.contour.feb <- rasterToContour(out.r1.raster.feb,levels=bbmm.contours.r1.feb5095$Z)
r1.raster.contour.feb <- spChFIDs(r1.raster.contour.feb,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.feb,dsn=".",layer="BBMMfeb (r150-95)",driver="ESRI Shapefile")

```

```

r1.raster.contour95.feb <- rasterToContour(out.r1.raster.feb,levels=bbmm.contours.r1.feb95$Z)
r1.raster.contour95.feb <- spChFIDs(r1.raster.contour95.feb,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.feb,dsn=".",layer="BBMMfeb (r195)",driver="ESRI Shapefile")

```

#MAR R1

```

out.r1.mar <- data.frame(x=bbmm.r1.mar$x,y=bbmm.r1.mar$y,z=bbmm.r1.mar$probability)
out.r1.raster.mar <- rasterFromXYZ(out.r1.mar,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.mar)
writeRaster(out.r1.raster.mar, 'r1 BBMMmar.tif')

```

```

r1.raster.contour.mar <- rasterToContour(out.r1.raster.mar,levels=bbmm.contours.r1.mar5095$Z)
r1.raster.contour.mar <- spChFIDs(r1.raster.contour.mar,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.mar,dsn=".",layer="BBMMmar (r150-95)",driver="ESRI Shapefile")

```

```

r1.raster.contour95.mar <- rasterToContour(out.r1.raster.mar,levels=bbmm.contours.r1.mar95$Z)
r1.raster.contour95.mar <- spChFIDs(r1.raster.contour95.mar,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.mar,dsn=".",layer="BBMMmar (r195)",driver="ESRI Shapefile")

```

#APR R1

```

out.r1.apr <- data.frame(x=bbmm.r1.apr$x,y=bbmm.r1.apr$y,z=bbmm.r1.apr$probability)
out.r1.raster.apr <- rasterFromXYZ(out.r1.apr,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.apr)
writeRaster(out.r1.raster.apr, 'r1 BBMMapr.tif')

```

```

r1.raster.contour.apr <- rasterToContour(out.r1.raster.apr,levels=bbmm.contours.r1.apr5095$Z)
r1.raster.contour.apr <- spChFIDs(r1.raster.contour.apr,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.apr,dsn=".",layer="BBMMapr (r150-95)",driver="ESRI Shapefile")

```

```

r1.raster.contour95.apr <- rasterToContour(out.r1.raster.apr,levels=bbmm.contours.r1.apr95$Z)
r1.raster.contour95.apr <- spChFIDs(r1.raster.contour95.apr,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.apr,dsn=".",layer="BBMMapr (r195)",driver="ESRI Shapefile")

```

```

#MAY R1
out.r1.may <- data.frame(x=bbmm.r1.may$x,y=bbmm.r1.may$y,z=bbmm.r1.may$probability)
out.r1.raster.may <- rasterFromXYZ(out.r1.may,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.may)
writeRaster(out.r1.raster.may, 'r1 BBMMmay.tif')

r1.raster.contour.may <- rasterToContour(out.r1.raster.may,levels=bbmm.contours.r1.may5095$Z)
r1.raster.contour.may <- spChFIDs(r1.raster.contour.may,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.may,dsn=".",layer="BBMMmay (r150-95)",driver="ESRI Shapefile")

r1.raster.contour95.may <- rasterToContour(out.r1.raster.may,levels=bbmm.contours.r1.may95$Z)
r1.raster.contour95.may <- spChFIDs(r1.raster.contour95.may,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.may,dsn=".",layer="BBMMmay (r195)",driver="ESRI Shapefile")

#JUN R1
out.r1.jun <- data.frame(x=bbmm.r1.jun$x,y=bbmm.r1.jun$y,z=bbmm.r1.jun$probability)
out.r1.raster.jun <- rasterFromXYZ(out.r1.jun,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r1.raster.jun)
writeRaster(out.r1.raster.jun, 'r1 BBMMjun.tif')

r1.raster.contour.jun <- rasterToContour(out.r1.raster.jun,levels=bbmm.contours.r1.jun5095$Z)
r1.raster.contour.jun <- spChFIDs(r1.raster.contour.jun,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour.jun,dsn=".",layer="BBMMjun (r150-95)",driver="ESRI Shapefile")

r1.raster.contour95.jun <- rasterToContour(out.r1.raster.jun,levels=bbmm.contours.r1.jun95$Z)
r1.raster.contour95.jun <- spChFIDs(r1.raster.contour95.jun,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r1.raster.contour95.jun,dsn=".",layer="BBMMjun (r195)",driver="ESRI Shapefile")

# 18.3 Create R2 raster and contour shapefiles:

#Annual r2
Annual_out.r2<- data.frame(x=bbmm.r2$x,y=bbmm.r2$y,z=bbmm.r2$probability)
Annual_out.r2.raster <- rasterFromXYZ(Annual_out.r2,crs=CRS("+init=epsg:3857"),digits=4)
plot(Annual_out.r2.raster)
writeRaster(Annual_out.r2.raster, 'Annual hr r2 .tif')

r2.raster.contour <- rasterToContour(Annual_out.r2.raster,levels=bbmm.contours.r25095$Z)
r2.raster.contour <- spChFIDs(r2.raster.contour,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour,dsn=".",layer="Annual BBMM (r250-95)",driver="ESRI Shapefile")

r2.raster.contour95 <- rasterToContour(Annual_out.r2.raster,levels=bbmm.contours.r295$Z)
r2.raster.contour95 <- spChFIDs(r2.raster.contour95,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour95,dsn=".",layer="Annual BBMM(r295)",driver="ESRI Shapefile")

r2.raster.contour50 <- rasterToContour(Annual_out.r2.raster,levels=bbmm.contours.r250$Z)
r2.raster.contour50 <- spChFIDs(r2.raster.contour50,paste(c(50),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour50,dsn=".",layer="Annual BBMM(r250)",driver="ESRI Shapefile")

#OCT r2
out.r2.oct <- data.frame(x=bbmm.r2.oct$x,y=bbmm.r2.oct$y,z=bbmm.r2.oct$probability)
out.r2.raster.oct <- rasterFromXYZ(out.r2.oct,crs=CRS("+init=epsg:3857"),digits=4)

```

```
plot(out.r2.raster.oct)
writeRaster(out.r2.raster.oct, 'r2 BBMMoct.tif')

r2.raster.contour.oct <- rasterToContour(out.r2.raster.oct, levels=bbmm.contours.r2.oct5095$Z)
r2.raster.contour.oct <- spChFIDs(r2.raster.contour.oct, paste(c(50,60,70,80,90,95), "% Contour Line", sep=""))
writeOGR(obj=r2.raster.contour.oct, dsn=".", layer="BBMMoct (r250-95)", driver="ESRI Shapefile")
#Note that with this given cell.size the layer of 50% and 60% are the same for jan r1, there are only 5 contours
created, while normally should be 6 contours
bbmm.contours.r2.oct5095 #Here is possibl to see that 50% and 60% have the same UD% and thus same value
and layer

r2.raster.contour95.oct <- rasterToContour(out.r2.raster.oct, levels=bbmm.contours.r2.oct95$Z)
r2.raster.contour95.oct <- spChFIDs(r2.raster.contour95.oct, paste(c(95), "% Contour Line", sep=""))
writeOGR(obj=r2.raster.contour95.oct, dsn=".", layer="BBMMoct (r295)", driver="ESRI Shapefile")

#NOV r2
out.r2.nov <- data.frame(x=bbmm.r2.nov$x, y=bbmm.r2.nov$y, z=bbmm.r2.nov$probability)
out.r2.raster.nov <- rasterFromXYZ(out.r2.nov, crs=CRS("+init=epsg:3857"), digits=4)
plot(out.r2.raster.nov)
writeRaster(out.r2.raster.nov, 'r2 BBMMnov.tif')

r2.raster.contour.nov <- rasterToContour(out.r2.raster.nov, levels=bbmm.contours.r2.nov5095$Z)
r2.raster.contour.nov <- spChFIDs(r2.raster.contour.nov, paste(c(50,60,70,80,90,95), "% Contour Line", sep=""))
writeOGR(obj=r2.raster.contour.nov, dsn=".", layer="BBMMnov (r250-95)", driver="ESRI Shapefile")

r2.raster.contour95.nov <- rasterToContour(out.r2.raster.nov, levels=bbmm.contours.r2.nov95$Z)
r2.raster.contour95.nov <- spChFIDs(r2.raster.contour95.nov, paste(c(95), "% Contour Line", sep=""))
writeOGR(obj=r2.raster.contour95.nov, dsn=".", layer="BBMMnov (r295)", driver="ESRI Shapefile")

#DEC r2
out.r2.dec <- data.frame(x=bbmm.r2.dec$x, y=bbmm.r2.dec$y, z=bbmm.r2.dec$probability)
out.r2.raster.dec <- rasterFromXYZ(out.r2.dec, crs=CRS("+init=epsg:3857"), digits=4)
plot(out.r2.raster.dec)
writeRaster(out.r2.raster.dec, 'r2 BBMMdec.tif')

r2.raster.contour.dec <- rasterToContour(out.r2.raster.dec, levels=bbmm.contours.r2.dec5095$Z)
r2.raster.contour.dec <- spChFIDs(r2.raster.contour.dec, paste(c(50,60,70,80,90,95), "% Contour Line", sep=""))
writeOGR(obj=r2.raster.contour.dec, dsn=".", layer="BBMMdec (r250-95)", driver="ESRI Shapefile")

r2.raster.contour95.dec <- rasterToContour(out.r2.raster.dec, levels=bbmm.contours.r2.dec95$Z)
r2.raster.contour95.dec <- spChFIDs(r2.raster.contour95.dec, paste(c(95), "% Contour Line", sep=""))
writeOGR(obj=r2.raster.contour95.dec, dsn=".", layer="BBMMdec (r295)", driver="ESRI Shapefile")

#JAN r2
out.r2.jan <- data.frame(x=bbmm.r2.jan$x, y=bbmm.r2.jan$y, z=bbmm.r2.jan$probability)
out.r2.raster.jan <- rasterFromXYZ(out.r2.jan, crs=CRS("+init=epsg:3857"), digits=4)
plot(out.r2.raster.jan)
writeRaster(out.r2.raster.jan, 'r2 BBMMjan.tif')

r2.raster.contour.jan <- rasterToContour(out.r2.raster.jan, levels=bbmm.contours.r2.jan5095$Z)
r2.raster.contour.jan <- spChFIDs(r2.raster.contour.jan, paste(c(50,60,70,80,90,95), "% Contour Line", sep=""))
```

```
writeOGR(obj=r2.raster.contour.jan,dsn=".",layer="BBMMjan (r250-95)",driver="ESRI Shapefile")

r2.raster.contour95.jan <- rasterToContour(out.r2.raster.jan,levels=bbmm.contours.r2.jan95$Z)
r2.raster.contour95.jan <- spChFIDs(r2.raster.contour95.jan,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour95.jan,dsn=".",layer="BBMMjan (r295)",driver="ESRI Shapefile")

#FEB r2
out.r2.feb <- data.frame(x=bbmm.r2.feb$x,y=bbmm.r2.feb$y,z=bbmm.r2.feb$probability)
out.r2.raster.feb <- rasterFromXYZ(out.r2.feb,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r2.raster.feb)
writeRaster(out.r2.raster.feb, 'r2 BBMMfeb.tif')

r2.raster.contour.feb <- rasterToContour(out.r2.raster.feb,levels=bbmm.contours.r2.feb5095$Z)
r2.raster.contour.feb <- spChFIDs(r2.raster.contour.feb,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour.feb,dsn=".",layer="BBMMfeb (r250-95)",driver="ESRI Shapefile")

r2.raster.contour95.feb <- rasterToContour(out.r2.raster.feb,levels=bbmm.contours.r2.feb95$Z)
r2.raster.contour95.feb <- spChFIDs(r2.raster.contour95.feb,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour95.feb,dsn=".",layer="BBMMfeb (r295)",driver="ESRI Shapefile")

#MAR r2
out.r2.mar <- data.frame(x=bbmm.r2.mar$x,y=bbmm.r2.mar$y,z=bbmm.r2.mar$probability)
out.r2.raster.mar <- rasterFromXYZ(out.r2.mar,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r2.raster.mar)
writeRaster(out.r2.raster.mar, 'r2 BBMMmar.tif')

r2.raster.contour.mar <- rasterToContour(out.r2.raster.mar,levels=bbmm.contours.r2.mar5095$Z)
r2.raster.contour.mar <- spChFIDs(r2.raster.contour.mar,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour.mar,dsn=".",layer="BBMMmar (r250-95)",driver="ESRI Shapefile")

r2.raster.contour95.mar <- rasterToContour(out.r2.raster.mar,levels=bbmm.contours.r2.mar95$Z)
r2.raster.contour95.mar <- spChFIDs(r2.raster.contour95.mar,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour95.mar,dsn=".",layer="BBMMmar (r295)",driver="ESRI Shapefile")

#APR r2
out.r2.apr <- data.frame(x=bbmm.r2.apr$x,y=bbmm.r2.apr$y,z=bbmm.r2.apr$probability)
out.r2.raster.apr <- rasterFromXYZ(out.r2.apr,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r2.raster.apr)
writeRaster(out.r2.raster.apr, 'r2 BBMMapr.tif')

r2.raster.contour.apr <- rasterToContour(out.r2.raster.apr,levels=bbmm.contours.r2.apr5095$Z)
r2.raster.contour.apr <- spChFIDs(r2.raster.contour.apr,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour.apr,dsn=".",layer="BBMMapr (r250-95)",driver="ESRI Shapefile")

r2.raster.contour95.apr <- rasterToContour(out.r2.raster.apr,levels=bbmm.contours.r2.apr95$Z)
r2.raster.contour95.apr <- spChFIDs(r2.raster.contour95.apr,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour95.apr,dsn=".",layer="BBMMapr (r295)",driver="ESRI Shapefile")

#MAY r2
out.r2.may <- data.frame(x=bbmm.r2.may$x,y=bbmm.r2.may$y,z=bbmm.r2.may$probability)
out.r2.raster.may <- rasterFromXYZ(out.r2.may,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r2.raster.may)
```

```

writeRaster(out.r2.raster.may, 'r2 BBMMmay.tif')

r2.raster.contour.may <- rasterToContour(out.r2.raster.may,levels=bbmm.contours.r2.may5095$Z)
r2.raster.contour.may <- spChFIDs(r2.raster.contour.may,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour.may,dsn=".",layer="BBMMmay (r250-95)",driver="ESRI Shapefile")

r2.raster.contour95.may <- rasterToContour(out.r2.raster.may,levels=bbmm.contours.r2.may95$Z)
r2.raster.contour95.may <- spChFIDs(r2.raster.contour95.may,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour95.may,dsn=".",layer="BBMMmay (r295)",driver="ESRI Shapefile")

#JUN r2
out.r2.jun <- data.frame(x=bbmm.r2.jun$x,y=bbmm.r2.jun$y,z=bbmm.r2.jun$probability)
out.r2.raster.jun <- rasterFromXYZ(out.r2.jun,crs=CRS("+init=epsg:3857"),digits=4)
plot(out.r2.raster.jun)
writeRaster(out.r2.raster.jun, 'r2 BBMMjun.tif')

r2.raster.contour.jun <- rasterToContour(out.r2.raster.jun,levels=bbmm.contours.r2.jun5095$Z)
r2.raster.contour.jun <- spChFIDs(r2.raster.contour.jun,paste(c(50,60,70,80,90,95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour.jun,dsn=".",layer="BBMMjun (r250-95)",driver="ESRI Shapefile")

r2.raster.contour95.jun <- rasterToContour(out.r2.raster.jun,levels=bbmm.contours.r2.jun95$Z)
r2.raster.contour95.jun <- spChFIDs(r2.raster.contour95.jun,paste(c(95),"% Contour Line",sep=""))
writeOGR(obj=r2.raster.contour95.jun,dsn=".",layer="BBMMjun (r295)",driver="ESRI Shapefile")

#The error "Error in spChFIDs(SL, x) : lengths differ" appears in oct R2 and jan r1 but doesn't seem to affect the
result and other cell.sizes are much more problematic...

```

2.2.2. CHOOSING CELL SIZE TO CALCULATE BBMM

In order to choose the cell size, track-logs from PB1 collected in April 2016 were used to produce raster layers with the “bbmm” package in R (R Core Team 2016) as described in chapter 2 with different cell sizes (in meters): 10,25,50,75, 100, 125, 150, 200. Then these layers were represented in QGIS (Quantum GIS Development Team 2017). A vector layer was added with waypoints of 11 encounters between R1 and PB1 in May, in which there were observers in both groups who marked the IGE starting point. Then this vector layer was overlapped with each raster layer. I counter counted in how many occasions the 2 points were in the same cell and thus, would have been representing the same intensity of use of space for both groups involved in the encounter (**Table I**).

Table I Cell sizes tested to calculate the home ranges by BBMMs employed in the project and the amount of paired points that fell in the same cell

Cell size (m)	Number of paired ige points in same cell	%
10	0	0
25	2	18.2
50	3	27.3
75	4	36.4
100	5	45.5
125	6	54.5
150	8	72.7
200	9	81.8

I chose the cell size 200 since all but two encounters fell into the same cell when using this size. However, when using 200 as a cell size the BBMM home range for some months could not be properly calculated. Since the errors varied depending on the cell size used, I tried several sizes around 200 (e.g. 199, 201, 198, etc) until I found one that produced all the layers needed without errors. This value was 190.

2.2.3. EXTRACTION OF INTENSITY OF USE VALUES IN QGIS

Step by step instructions on how I extracted the values of intensity of use for each intergroup encounter location in QGIS (Modified from instructions provided by James Waterman):

1. Open the BBMM rasters (.tiff) needed using "Add Raster Layer". Files will be located in the current R working directory.
2. Normalise rasters: Open 'Processing Toolbox' > 'SAGA' > 'Raster calculus' > 'Raster normalisation'. Then chose: Grid = "Your new clipped raster layer"; Target range (min) = 0; Target Range (max) = 100.
3. Run and save the resulted layer with the appropriate CRS (Coordinate Reference System)
4. Import the IGE locations in the original format (.gpx) to QGIS using the GPS Tool (GPS plugin). Save them with the appropriate CRS.
5. Open 'Processing Toolbox' > 'SAGA' > 'Vector to raster' > 'Add raster values to points'
6. Then choose: Points = "Your intergroup encounter points"; Grids = "layer created in step 3" Interpolation = 'Nearest Neighbour'. Press run and save
7. Open the point layer generated in step 6 'Layers Panel' > 'Open Attribute Table'.
8. Those are the values of the intensity of use of the intergroup encounter location

2.2.4. EXTRACTION OF DISTANCE TO CORE AREA VALUES IN QGIS

1. Calculate in R the 50% BBMM contours (See: 2.2.1)
2. In QGIS, import the contours (.shp) as vector layers and transform them into polygons (Vector>Geometry tools> Layers to polygons)
3. Import the IGE points and project them into the proper CRS
4. Install NNJoin plugin
5. In NNJoin plugin, add first the IGEs and then the polygon of the core area of the group and month you want to calculate and run
6. The distance will be found in the attribute table of the IGE point layer

2.3. R Scripts of models predicting the probability of intergroup outcome and intensity in crested macaques considering differences in group size and location-based payoffs.

2.3.1. MODELS PREDICTING THE PROBABILITY OF DECIDED INTERGROUP ENCOUNTER

```
## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr

# using the package:
updateR() # This will start the updating process of your R installation.
# It will check for newer versions, and if one is available, will guide you through the decisions you'd need to
make.

## download packages
install.packages("lme4") #Package that allows to calculate the glms
```

```
#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()
```

```
## Upload data
factors_original<-read.csv("factors_originalv1.csv")
```

Appendix from: L.Martínez-Íñigo. 2018. Ph.D. Thesis. Intergroup interactions in crested macaques.

```
#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison
cannot be made)
#<<values that are missing only for certain variables change the data set and sample size, depending on which
variable is included in
# any given model. I suggest to remove missing cases before starting model selection>> Mazerolle 2017.
```

```
missingrows = is.na(factors_original$abs_groupsize)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$decided_undecided)
factors_original= factors_original[!missingrows,]
```

```
cat("\n\n\n\n\n Checking potential control variables \n\n\n\n\n")
```

```
cat("\n\n\ Duration and number of observers \n\n")
```

```
resdu_cv=glmer(decided_undecided ~ duration|GE+num_obs+ (1|dyad), family="binomial",
data=factors_original)
```

```
print(summary(resdu_cv))
```

```
#Comparison between the null model and the model with duration as a fixed factor
resdu.null=glmer(decided_undecided ~ 1 +(1| dyad), family="binomial", data=factors_original)
print(summary(resdu.null))
```

```
print(anova(resdu.null,resdu_cv, test="Chisq"))
```

```
#No possible control variable is significant and therefore, none will be used.
```

```
#Starting a list to calculate AICs to compare between all the models
models<-list()
models[[1]]<-resdu.null
Modnames <- "Null model"
```

```
#Calculating R2
r2_null<-r.squaredGLMM(resdu.null)
```

```
R2_und<-r2_null
```

```
cat("\n\n\n\n\n\ Use of space and relative group size \n\n\n\n\n")
```

```
cat("\n\n\n\n\ Models with UD \n\n\n\n\n")
```

```
#####Group size and absolute use of space #####
# Following Roths and Cords 206 p.50 "In addition, we predicted that the odds of a draw would be higher (1)
when groups were more similar in size, (2) when site
```

```
# occupancy was more symmetrical and (3) when contests occurred at sites that were similarly central in both groups' home ranges. As before, we evaluated site occupancy for multiple periods before each contest."
```

```
#Checking colinearity
vif(glm(decided_undecided ~abs_UD190 +abs_groupsize,family="binomial", data=factors_original))
```

```
#Run the model (with interactions)
resdu_gud0=glmer(decided_undecided ~
  abs_groupsize +
  abs_UD190+
  abs_groupsize*abs_UD190+
  (1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resdu_gud0))
```

```
cat("\n\n\n Comparison of Group size & absolute difference in use of space Model to null model\n\n")
print(anova(resdu.null,resdu_gud0, test="Chisq"))
```

```
#Run the model (without interactions)
resdu_gud=glmer(decided_undecided ~
  abs_groupsize +
  abs_UD190+
  (1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resdu_gud))
```

```
cat("\n\n\n Comparison of Group size & absolute difference in use of space Model to null model\n\n")
print(anova(resdu.null,resdu_gud, test="Chisq"))
```

```
#Including model in AIC list
models[[2]]<-resdu_gud
Modnames<-rbind(Modnames, "Full model gs+absUD model")
```

```
#Calculating R2
```

```
r2_full_gsabsUD<-r.squaredGLMM(resdu_gud)
R2_und<-rbind(R2_und,r2_full_gsabsUD)
```

```
xlabels<-c("' Relative group size' (No. individuals) ", "' Relative use of the area where the encounter starts' (ST.UD)")
```

```
plotLMER.fnc(resdu_gud,ylim=0:1,lockYlim=TRUE,linecolor="black",
  lwd=4,xlabs=xlabels,
  ylabel="Probability of decided encounter")
```

```
###GROUP SIZE, BUT NO ABS UD190 WAS A SIGNIFICANT VARIABLE. THEREFORE, A MODEL JUST WITH  
ABS_GROUPSIZE WAS RUN
```

```
resdu_gs=glmer(decided_undecided ~  
               abs_groupsize+  
               (1|dyad), family="binomial", data=factors_original)  
  
print(summary(resdu_gs))
```

```
cat("\n\n\n Comparison of Group size Model to null model\n\n")  
print(anova(resdu.null,resdu_gs, test="Chisq"))
```

```
#Including model in AIC list  
models[[3]]<-resdu_gs  
Modnames<-rbind(Modnames, "Group size model")
```

```
#Calculating R2
```

```
r2_groupsize<-r.squaredGLMM(resdu_gs)  
R2_und<-rbind(R2_und,r2_groupsize)
```

```
plotLMER.fnc(resdu_gs,ylimit=0:1,lockYlim=TRUE,linecolor="black",  
             lwd=4,xlabel="Absolute difference in group size",  
             ylabel="Probability of decided encounter")
```

```
cat("\n\n\n Is this result due to the 2 cases on encounter bewteen r2 and pb1? \n\n\n")
```

```
nopb1r2<-factors_original[factors_original$dyad!="pb1r2",]  
resdu.null2=glmer(decided_undecided ~ 1+ (1|dyad), family="binomial", data=nopb1r2)  
print(summary(resdu.null2))
```

```
#Starting a list to calculate AICs to compare between all the models  
models_nopb1r2<-list()  
models_nopb1r2[[1]]<-resdu.null2  
Modnames_nopb1r2 <- "Null model"
```

```
#Calculating R2  
r2_null_nopb1r2<-r.squaredGLMM(resdu.null2)  
R2_nopb1r2<-r2_null_nopb1r2
```

```
#Group size+ Use of space  
resdu_gud2=glmer(decided_undecided ~  
                abs_groupsize +
```

```

abs_UD190+
(1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_gud2))

cat("\n\n\n Comparison of Group size & absolute difference in use of space Model to null model\n\n")
print(anova(resdu.null2,resdu_gud2, test="Chisq"))

#Including model in AIC list
models_nopb1r2[[2]]<-resdu_gud2
Modnames_nopb1r2<-rbind(Modnames_nopb1r2, "Full model gs+absUD model")

#Calculating R2

r2_gsabsUD_nopb1r2<-r.squaredGLMM(resdu_gud2)
R2_nopb1r2<-rbind(R2_nopb1r2,r2_gsabsUD_nopb1r2)

xlabels<-c("'Relative group size' (No. individuals) ", "'Relative use of the area where the encounter starts' (ST.UD)")

plotLMER.fnc(resdu_gud2,ylim=0:1,lockYlim=TRUE,linecolor="black",
             lwd=4,xlabs=xlabels,
             ylabel="Probability of decided encounter(no pb1r2)")

#####Use of space by Quartiles#####

first_quartile<-factors_original[factors_original$quartile_UD=="1",]
summary(first_quartile$dyad)

# Data: first_quartile (1st quartile of sum_UD)
# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Fixed effect: abs_UD190 (UD190_G1- UD190_G2) and abs_UD190
# Random effect: 'dyad', 2 levels (the IGE pb1r2 are not within this quartile)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was low (25% lowest of the sample), so when both groups had a
# low use of the area, it would be expected that the higher abs_UD190, the higher the probability of a decided encounter (otherwise if both
# use the area little more or less equally, they may not fight nor leave). Then, the lower the differences in group size, the more likely
# a the encounter would be to be undecided

#Checking colinearity
vif(glm(decided_undecided ~ abs_UD190 +abs_groupsize,family="binomial", data=first_quartile))

#Run the model(with interactions)
resdu_qud1gs0=glmer(decided_undecided ~
                    abs_UD190 +
                    abs_groupsize+abs_UD190*abs_groupsize+(1|dyad), family="binomial", data=first_quartile)

print(summary(resdu_qud1gs0))

```

```
#Run the model
resdu_qud1gs=glmer(decided_undecided ~
  abs_UD190 +
  abs_groupsize+(1|dyad), family="binomial", data=first_quartile)

print(summary(resdu_qud1gs))

cat("\n\n\n Comparison of 1st quartile sum_UD & group size model to null model\n\n")
resdu.null1q<-glmer(decided_undecided ~ 1+(1|dyad), family="binomial", data=first_quartile)
print(anova(resdu.null1q,resdu_qud1gs, test="Chisq"))

plotLMER.fnc(resdu_qud1gs,ylimit=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="Groups size and 1Q UD",
  ylabel="Probability of decided encounter-1st quartile sum_UD")

# Data: third_quartile 3rd quartile of sum_UD
# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Fixed effect: abs_UD190 (UD190_G1- UD190_G2) and abs_group size
# Random effect: 'dyad', 2 levels (the IGE pb1r2 are not within this quartile)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was high (25% highest of the
sample), it would
# be expected no effect on outcome, since independently of abs_UD190, one or both groups would highly value
the resource and
# there would be winner(highe abs_UD190), either by one retreating or by fighting until one is defeated. The
more similar the
# group sizes, the more likely the encounter would be to be undecided.
third_quartile<-factors_original[factors_original$quartile_UD=="3",]
summary(third_quartile$dyad)

#Checking colinearity
vif(glm(decided_undecided ~ abs_UD190 +abs_groupsize,family="binomial", data=third_quartile))

#Run the model
resdu_qud3gs0=glmer(decided_undecided ~
  abs_UD190 +
  abs_groupsize+abs_UD190*abs_groupsize+
  (1|dyad), family="binomial", data=third_quartile)

print(summary(resdu_qud3gs0))

#Run the model
resdu_qud3gs=glmer(decided_undecided ~
  abs_UD190 +
  abs_groupsize+
  (1|dyad), family="binomial", data=third_quartile)

print(summary(resdu_qud3gs))
```

```
cat("\n\n Comparison of Q3 sum_ud190 & group size model to null model\n\n")
resdu.null3q<-glmer(decided_undecided ~ 1+(1|dyad), family="binomial", data=third_quartile)
print(anova(resdu.null3q,resdu_qud3gs, test="Chisq"))

plotLMER.fnc(resdu_qud3gs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="abs(relative use)",
             ylabel="Probability of decided encounter-3rd quartile sum_UD")

#####Low VS High use of space#####

# Data: low_absUD_quartiles
# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Fixed effect: quartile_UD (categorical) and abs_groupsize
# Random effect: 'dyad', 2 levels (the IGE pb1r2 are not within this category)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was high (25% highest of the
sample) or low(25% lowest of the sample) ,
# and where differences in usage between the groups are low (only the lowest third of data of abs_UD190 were
selected), we would expect Q1 to have a
# significantly lower probability of decided encounter than the Q3. Then, the higher the relative group size, the
higher the chances of decided
# encounter
quartiles1and3<-factors_original[factors_original$quartile_UD!="2",] #Take only the 1st and 3rd quartiles of
sum_UD
low_absUD_quartiles<-quartiles1and3[quartiles1and3$excl_quartilesUD=="1",] #From the previous result, take
only the ones with low abs_UD
summary(low_absUD_quartiles$dyad)

#Run the model quartiles (with interactions)
resdu_udqgs0=glmer(decided_undecided ~
                  quartile_UD +
                  abs_groupsize+quartile_UD*abs_groupsize+
                  (1|dyad), family="binomial", data=low_absUD_quartiles)

print(summary(resdu_udqgs0))

#Run the model quartiles
resdu_udqgs=glmer(decided_undecided ~
                  quartile_UD +
                  abs_groupsize+
                  (1|dyad), family="binomial", data=low_absUD_quartiles)

print(summary(resdu_udqgs))

cat("\n\n Comparison of UD quartile model to null model\n\n")
```

```
resdu.nullq<-glmer(decided_undecided ~ 1+(1|dyad), family="binomial", data=low_absUD_quartiles)
print(anova(resdu.nullq,resdu_udqgs, test="Chisq"))

plotLMER.fnc(resdu_udqgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Quartiles",
             ylabel="Probability of decided encounter")

cat("\n\n\n\n Models with core area \n\n\n\n\n")

cat("\n\n\n\n Absolute distance to core area and group size \n\n\n\n\n")

#Following Roths & Cords 2016 we predicted that the odds of a draw would be higher (1) when groups were
more similar in size, (2) when site
# occupancy was more symmetrical and (3) when contests occurred at sites that were similarly central in both
groups' home ranges.
#Checking colinearity

vif(glm(decided_undecided ~ abs_distancetocorearea+abs_groupsize,family="binomial", data=factors_original))

#Run the model(with interactions)
resdu_dsgs0=glmer(decided_undecided ~
                 abs_distancetocorearea+
                 abs_groupsize+abs_groupsize*abs_distancetocorearea+
                 (1|dyad), family="binomial", data=factors_original)

print(summary(resdu_dsgs0))

cat("\n\n\n\n Comparison of Group size & core area Model to null model\n\n\n")
print(anova(resdu.null,resdu_dsgs0, test="Chisq"))

#Run the model(without interactions)
resdu_dsgs=glmer(decided_undecided ~
                 abs_distancetocorearea+
                 abs_groupsize+
                 (1|dyad), family="binomial", data=factors_original)

print(summary(resdu_dsgs))

cat("\n\n\n\n Comparison of Group size & core area Model to null model\n\n\n")
print(anova(resdu.null,resdu_dsgs, test="Chisq"))

#The model is significantly different although no variable itself is significant. The full model is kept
```

```
#Including model in AIC list
models[[4]]<-resdu_dsgs
Modnames<-rbind(Modnames, "Group size + abs distance to core model")

#Calculating R2

r2_dsgs<-r.squaredGLMM(resdu_dsgs)
R2_und<-rbind(R2_und,r2_dsgs)

xlabels<-c("' Relative distance to the closest core area' (meters)", "' Relative group size' (No. individuals)")
plotLMER.fnc(resdu_dsgs,ylimit=0:1,lockYlim=TRUE,linecolor="black",
             lwd=4,xlabs=xlabels,
             ylabel="Probability of decided encounter")

cat("\n\n\n Is this result due to the 2 cases on encounter bewteen r2 and pb1? \n\n\n")

#Run the model
resdu_dsgs2=glmer(decided_undecided ~
                 abs_distancetocorearea+
                 abs_groupsize+
                 (1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_dsgs2))

cat("\n\n\n Comparison of Group size & core area Model to null model\n\n\n")
print(anova(resdu.null2,resdu_dsgs2, test="Chisq"))

#Including model in AIC list
models_nopb1r2[[3]]<-resdu_dsgs2
Modnames_nopb1r2<-rbind(Modnames_nopb1r2, "Full model gs+abs dis model")

#Calculating R2

r2_dsgs_nopb1r2<-r.squaredGLMM(resdu_dsgs2)
R2_nopb1r2<-rbind(R2_nopb1r2,r2_dsgs_nopb1r2)

xlabels<-c("' Relative distance to the closest core area' (meters)", "' Relative group size' (No. individuals) ")
plotLMER.fnc(resdu_dsgs2,ylimit=0:1,lockYlim=TRUE,linecolor="grey41",
             lwd=4,xlabs= xlabels,
             ylabel="Probability of decided encounter (no pb1r2)")

plot(x = factors_original$abs_groupsize,
     y = factors_original$decided_undecided,
     xlab = "' Relative group size' (No. individuals)",
```

```
ylab = "Draw (0) VS Decided (1)")

plot(x = nopb1r2$abs_groupsize,
     y = nopb1r2$decided_undecided,
     xlab = "'Relative group size' (No. individuals)",
     ylab = "Draw (0) VS Decided (1)")

cat("\n\n\n Categorical core area and group size \n\n\n")

# Response: decided_undecided (binary, 1=Decided IGE, 0=Undecided IGE)
# Fixed effect: core_yn (y=1 group was in its core area, n= no group was in its core area, b=both groups were in
a core area) and abs_groupsize
# Random effect: 'dyad', 3 levels.
# Hypothesis: Decided encounters will be more likely when one (y) or both(b) groups are in their core area, and
the least when none is in the core
# area. Also, the more similar the group sizes, the more likely the encounter would be to end undecided

#Checking colinearity
vif(glm(decided_undecided ~ core_yn + abs_groupsize, family="binomial", data=factors_original))

#Run the model (with interactions)
resdu_cyngs0=glmer(decided_undecided ~
  core_yn +
  abs_groupsize+core_yn*abs_groupsize+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resdu_cyngs0))

cat("\n\n\n Comparison of Group size & core area Model to null model\n\n\n")
print(anova(resdu.null,resdu_cyngs0, test="Chisq"))

#Run the model (without interactions)
resdu_cyngs=glmer(decided_undecided ~
  core_yn +
  abs_groupsize+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resdu_cyngs))

cat("\n\n\n Comparison of Group size & core area Model to null model\n\n\n")
print(anova(resdu.null,resdu_cyngs, test="Chisq"))

#Including model in AIC list
models[[5]]<-resdu_cyngs
Modnames<-rbind(Modnames, "Group size + in-out core area")
```

```

#Calculating R2
r2_cyngs<-r.squaredGLMM(resdu_cyngs)
R2_und<-rbind(R2_und,r2_cyngs)

xlabels<-c("'Encounter location'", "'Relative group size' (No. individuals)")
plotLMER.fnc(resdu_cyngs,ylim=0:1,lockYlim=TRUE,linecolor="black",
             lwd=4,xlabs=xlabels,
             ylabel="Probability of decided encounter")

####GROUP SIZE, BUT NO CORE YN WAS A SIGNIFICANT VARIABLE, SAME AS WITH GROUP SIZE AND UD, NO
ADJUSTED MODEL GENERATED

cat("\n\n\n Is this result due to the 2 cases on encounter bewteen r2 and pb1? \n\n\n")

resdu_cyngs2=glmer(decided_undecided ~
                  core_yn +
                  abs_groupsize+
                  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_cyngs2))

cat("\n\n\n Comparison of Group size & core area Model to null model\n\n")
print(anova(resdu.null2,resdu_cyngs2, test="Chisq"))

#Including model in AIC list
models_nopb1r2[[4]]<-resdu_cyngs2
Modnames_nopb1r2<-rbind(Modnames_nopb1r2, "Full model gs+categorical cores model")

#Calculating R2
r2_cyngs_nopb1r2<-r.squaredGLMM(resdu_cyngs2)
R2_nopb1r2<-rbind(R2_nopb1r2,r2_cyngs_nopb1r2)

xlabels<-c("'Encounter location'", "'Relative group size' (No. individuals)")
plotLMER.fnc(resdu_cyngs2,ylim=0:1,lockYlim=TRUE,linecolor="black",
             lwd=4,xlabs=xlabels,
             ylabel="Probability of decided encounter (no pb1r2)")

cat("\n\n\n\n\n Distance to core area by quartiles & Group size \n\n\n\n\n")

# Data: first_quartile dis (1st quartile of sum_distancetocorearea)
# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Fixed effect: abs_distancetocorearea (abs(distancetocorearea_G1- distancetocorearea_G2)) + abs_groupsize
# Random effect: 'dyad', 2 levels (no pb1r2 IGEs in this category)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was low (25%
lowest of the sample), so when
# both groups were close to their core area, it would be expected a high overall probability of decided
encounters, higher the smaller
# the abs_distancetocorearea The more similar the group size, the less likely the encounter has to be decided.
The more similar the
# group sizes, the more likely the encounter would be to be undecided

```

```

first_quartiledis<-factors_original[factors_original$quartile_dist=="1",]
summary(first_quartiledis$dyad)

vif(glm(decided_undecided ~ abs_distancetocorearea+abs_groupsize, family="binomial",
data=first_quartiledis))

#Run the model
resdu_q1disgs=glmer(decided_undecided ~ abs_groupsize+abs_distancetocorearea+
abs_distancetocorearea*abs_groupsize +(1| dyad), family="binomial", data=first_quartiledis)

print(summary(resdu_q1disgs))

table(first_quartiledis$decided_undecided)

cat("\n\n\n Comparison of 1st quartile of sum_distancetocorearea model to null model\n\n")
resdu.null1qdis<-glmer(decided_undecided ~ 1 +(1| dyad), family="binomial", data=first_quartiledis)
summary(resdu.null1qdis)
print(anova(resdu.null1qdis,resdu_q1disgs, test="Chisq"))

#Creating AUCc tab
models2<-list()
models2[[1]]<-resdu.null1qdis
Modnames2 <- "Null model"
models2[[2]]<-resdu_q1disgs
Modnames2 <- rbind(Modnames2,"Full Q1 (int.)")

#Calculating R2
r2_null1qdis<-r.squaredGLMM(resdu.null1qdis)
R2_2<-r2_null1qdis

r2_1qdis<-r.squaredGLMM(resdu_q1disgs)#Cant be calculated
R2_2<-rbind(R2_2,r2_1qdis)

plotLMER.fnc(resdu_q1disgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,xlabel="abs(relative distance to core area)",
ylabel="Probability of decided encounter-1st quartile")

##Data for interaction graph
first_quartiledis$abs_groupsize
first_quartiledis$abs_distancetocorearea

# Data: third_quartile 3rd quartile of sum_distancetocorearea
# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Fixed effect: abs_distancetocorearea (abs(distancetocorearea_G1- distancetocorearea_G2))+abs_groupsize
# Random effect: 'dyad', 3 levels.
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was high (25%
highest of the sample), it would be
# expected that the higher the difference (i.e. abs_distancetocorearea), the higher the probabilities of a decided
encounter

```

```

# (one would have more reasons to fight and the other to withdraw), but an overall high probability of
undecided. The more similar the group
# sizes, the more likely the encounter would be to be undecided
third_quartiledis<-factors_original[factors_original$quartile_dist=="3",]
summary(third_quartiledis$dyad)

vif(glm(decided_undecided ~ abs_distancetocorearea+abs_groupsize, family="binomial",
data=third_quartiledis))

#Run the model(with interactions)
resdu_q3disgs0=glmer(decided_undecided ~
  abs_distancetocorearea +abs_groupsize+abs_distancetocorearea*abs_groupsize+
  (1|dyad), family="binomial", data=third_quartiledis)

print(summary(resdu_q3disgs0))

#Run the model
resdu_q3disgs=glmer(decided_undecided ~
  abs_distancetocorearea +abs_groupsize+
  (1|dyad), family="binomial", data=third_quartiledis)

print(summary(resdu_q3disgs))

cat("\n\n\n Comparison of Q3 Sum_distancetocorearea +group size model to null model\n\n")
resdu.null3qdis<-glmer(decided_undecided ~ 1 +(1|dyad), family="binomial", data=third_quartiledis)
print(anova(resdu.null3qdis,resdu_q3disgs, test="Chisq"))

plotLMER.fnc(resdu_q3disgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="abs(relative distance to core area)",
  ylabel="Probability of decided encounter-3rd quartile")

cat("\n\n\n\n\n Close to Core VS Far From Core\n\n\n\n")

# Data: quartiles_dist
# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Fixed effect: quartiles of distance to core area (Q1=close to core area (low_sum), Q3=Far from core area)
+abs_groupsize
# Random effect: 'dyad', 3 levels.
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was high (25%
highest of the sample) or
# low(25% lowest of the sample) , we would expect Q1 to have significantly higher chances of decided encounter
than the Q3, if we use
# quartiles as fixed effect. The more similar the group sizes, the more likely the encounter would be to be
undecided.

quartiles_dist<-factors_original[factors_original$excl_quartilesDist=="1",] #Take the Q1 and Q3 of
sum_distant to core area
summary(quartiles_dist$dyad)

vif(glm(decided_undecided ~ abs_distancetocorearea+abs_groupsize, family="binomial", data=quartiles_dist))

```

```
#Run the model quartiles (with inteactions)
resdu_disqgs0=glmer(decided_undecided ~
                    quartile_dist +abs_groupsize+quartile_dist*abs_groupsize+
                    (1|dyad), family="binomial", data=quartiles_dist)

print(summary(resdu_disqgs0))

#Run the model quartiles
resdu_disqgs=glmer(decided_undecided ~
                    quartile_dist +abs_groupsize+
                    (1|dyad), family="binomial", data=quartiles_dist)

print(summary(resdu_disqgs))

cat("\n\n\n Comparison of Q1 and Q3 of distance to core area + group size model to null model\n\n")

resdu.nullqdis<-glmer(decided_undecided ~ 1+ (1|dyad), family="binomial", data=quartiles_dist)
print(summary(resdu.nullqdis))
print(anova(resdu.nullqdis,resdu_disqgs, test="Chisq"))

plotLMER.fnc(resdu_disqgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Quartiles distance",
             ylabel="Probability of decided encounter")

models3<-list()
models3[[1]]<-resdu.nullqdis
Modnames3 <- "Null model"
models3[[2]]<-resdu_disqgs
Modnames3 <- rbind(Modnames3,"Full Q1vsQ3 dis")

#Calculating R2
r2_nullqdis<-r.squaredGLMM(resdu.nullqdis)
R2_3<-r2_nullqdis

r2_disqgs<-r.squaredGLMM(resdu_disqgs)
R2_3<-rbind(R2_3,r2_disqgs)

###Group size does not have an effect but quartiles does, so a new model is run with only this variable

#Run the model quartiles
resdu_disq=glmer(decided_undecided ~
                 quartile_dist+
                 (1|dyad), family="binomial", data=quartiles_dist)

print(summary(resdu_disq))

cat("\n\n\n Comparison of Q1 and Q3 of distance to core area + group size model to null model\n\n")
print(anova(resdu.nullqdis,resdu_disq, test="Chisq"))
```

```

plotLMER.fnc(resdu_disq,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Quartiles distance",
             ylabel="Probability of decided encounter")

models3[[3]]<-resdu_disq
Modnames3 <- rbind(Modnames3,"Q1vsQ3 dis")

#Calculating R2
r2_disq<-r.squaredGLMM(resdu_disq)
R2_3<-rbind(R2_3,r2_disq)

####Is this due to the 2 encounters between pb1 and r2?

quartiles_disq2<-nopb1r2[nopb1r2$excl_quartilesDist == "1",] #Take the Q1 and Q3 of sum_distante to core
area
summary (quartiles_disq2$dyad)

vif(glm(decided_undecided ~ abs_distancetocorearea+abs_groupsize, family="binomial", data=quartiles_disq2))

#Run the model quartiles
resdu_disq2=glmer(decided_undecided ~
                  quartile_dist +
                  (1|dyad), family="binomial", data=quartiles_disq2)

print(summary(resdu_disq2))

cat("\n\n\n Comparison of Q1 and Q3 of distance to core area + group size model to null model\n\n")
resdu.nullqdis2<-glmer(decided_undecided ~ 1+ (1|dyad), family="binomial", data=quartiles_disq2)
print(anova(resdu.nullqdis2,resdu_disq2, test="Chisq"))

plotLMER.fnc(resdu_disq,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Quartiles distance",
             ylabel="Probability of decided encounter")

cat("\n\n\n\n\n\n\n\n\n SUMMARY OF RESULTS\n\n\n\n\n\n\n\n\n")

#Models with full dataset (129 IGEs)
R2_und

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)

#I don't find any way of changing the graph labels, so it'll have to be done by hand :(

sjp.glmer(resdu_gud, type="pred", facet.grid=FALSE, vars="abs_UD190",
          geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resdu_gud, type="pred", facet.grid=FALSE, vars="abs_groupsize",
          geom.colors = "bw",show.ci=TRUE)

```

```

sjp.glmer(resdu_dsgs, type="pred", facet.grid=FALSE, vars="abs_distancetocorearea",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resdu_dsgs, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resdu_cyngs, type="pred", facet.grid=FALSE, vars="core_yn",
  geom.colors = "bw",show.ci=TRUE)#DOesn't make much sense, but I cannot leabe only the points

sjp.glmer(resdu_cyngs, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)

#Models with without pb1r2 (127 IGEs)

R2_nopb1r2

aictab(cand.set=models_nopb1r2, modnames = Modnames_nopb1r2, second.ord = TRUE, nobs = NULL, sort =
TRUE)

sjp.glmer(resdu_gud2, type="pred", facet.grid=FALSE, vars="abs_UD190",
  geom.colors = "bw"),show.ci=TRUE

sjp.glmer(resdu_gud2, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resdu_dsgs2, type="pred", facet.grid=FALSE, vars="abs_distancetocorearea",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resdu_dsgs2, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw", show.ci=TRUE)

#Models comparing Q1 dis. (35 IGEs)
aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)

R2_2#The model didn't converge

sjp.glmer(resdu_q1disgs, type="pred",facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw")
sjp.glmer(resdu_q1disgs, type="pred",facet.grid=FALSE, vars="abs_distancetocorearea",
  geom.colors = "bw")

table(first_quartiledis$dysad,
  first_quartiledis$decided_undecided)

plot(x = first_quartiledis$abs_groupsize,
  y = first_quartiledis$abs_distancetocorearea,
  xlab = "Absolute group size",
  ylab = "Absolute distance to core")

M0 <- lm(durationIGE~abs_groupsize, data = first_quartiledis)
abline(M0, lwd = 3)

```

```
summary (M0)
```

```
ggplot(first_quartiledis, aes(x=dyad,y=abs_distancetocorearea))+  
  geom_boxplot()+  
  facet_wrap(~decided_undecided)
```

```
#Models comparing Q1 vs Q3 dis. (64 IGEs)
```

```
aictab(cand.set=models3, modnames = Modnames3, second.ord = TRUE, nobs = NULL, sort = TRUE)
```

```
R2_3
```

```
#With PB1-R2
```

```
sjp.glmer(resdu_disq, type="pred", facet.grid=FALSE, vars="quartile_dist",  
  geom.colors = "bw",show.ci=TRUE)
```

```
#Without PB1-R2
```

```
sjp.glmer(resdu_disq2, type="pred", facet.grid=FALSE, vars="quartile_dist",  
  geom.colors = "bw",show.ci=TRUE)
```

```
cat("\n\n\n What variability does dyad explain? \n\n\n")
```

```
resdu_dy=glm(decided_undecided ~ dyad, family="binomial", data=factors_original)  
resdu.nulldy=glm(decided_undecided ~ 1, family="binomial", data=factors_original)
```

```
print(summary(resdu_dy))
```

```
cat("\n\n\n Comparison between dyad model and null model\n\n\n")
```

```
print(anova(resdu.nulldy,resdu_dy, test="Chisq"))
```

```
#Calculate (pseudo) R-squared statistics
```

```
RsqGLM(resdu_dy)
```

```
cat("\n\n\n What variability does dyad explain without pb1r2? \n\n\n")
```

```
resdu_dy2=glm(decided_undecided ~ dyad, family="binomial", data=nopb1r2)  
resdu.nulldy2=glm(decided_undecided ~ 1, family="binomial", data=nopb1r2)
```

```
print(summary(resdu_dy2))
```

```
cat("\n\n Comparison between dyad model and null model\n\n")

print(anova(resdu.nulldy2,resdu_dy2, test="Chisq"))

#Calculate (pseudo) R-squared statistics

RsqGLM(resdu_dy2)
```

2.3.2. MODELS PREDICTING THE PROBABILITY OF WINING AN ENCOUNTER

```
## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr

# using the package:
updateR() # this will start the updating process of your R installation. It will check for newer versions, and if one
is available, will guide you through the decisions you'd need to make.

install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ppcor")#To check for correlations between independent variables
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the fata points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine

library(lme4)
library(car)
library(ppcor)
library(ggplot2)
library(modEvA)
library(languageR)
library(AICcmodavg)
library(MuMIn)
library(sjPlot)
library(dplyr)

#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
```

```
getwd()

## Upload data
factors_original<-read.csv("factors_originalv1.csv")

cat("\n\n\n Is there intergroup dominance? \n\n")
# R1 won 55 IGEs to PB1 of 85 decided IGEs
# R1 won 17 IGEs to R2 of 43 decided IGEs
# No decided IGEs PB1-R2

#R1-PB1
binom.test(55, 85, p = 0.5,
           alternative = c("two.sided", "less", "greater"),
           conf.level = 0.95)
binom.test(30, 85, p = 0.5,
           alternative = c("two.sided", "less", "greater"),
           conf.level = 0.95)

#R1-R2

binom.test(17, 43, p = 0.5,
           alternative = c("two.sided", "less", "greater"),
           conf.level = 0.95)
binom.test(26, 43, p = 0.5,
           alternative = c("two.sided", "less", "greater"),
           conf.level = 0.95)

#### Flip the variables for pb1-r1 so R1 is the focal group in all the encounters with decided outcome

#Checking the original data
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_groupsize[factors_original$dyad=="pb1r1"]
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"]

#Flipping pb1-r1 to r1-pb1
factors_original$winner_analysis[ factors_original$dyad=="pb1r1"] <-1-factors_original$winner_analysis[
factors_original$dyad=="pb1r1"]
factors_original$rel_groupsize[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_groupsize[
factors_original$dyad=="pb1r1"]
factors_original$rel_UD190[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_UD190[factors_original$dyad=="pb1r1"]
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"]

#Checking that the flipping worked
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_groupsize[factors_original$dyad=="pb1r1"]
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"]
```

```
####Convert variables to the appropriate format
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$winner_analysis<- factor(factors_original$winner_analysis)
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$rel_groupsize<- as.numeric(factors_original$rel_groupsize)
factors_original$rel_UD190<- as.numeric(factors_original$rel_UD190)
factors_original$rel_distancetocorearea<- as.numeric(factors_original$rel_distancetocorearea)

summary(factors_original$durationIGE)

#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison
cannot be made)
#<<values that are missing only for certain variables change the data set and sample size, depending on which
variable is included in
# any given model. I suggest to remove missing cases before starting model selection>> Mazerolle 2017.

missingrows = is.na(factors_original$rel_groupsize)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$winner_analysis)
factors_original= factors_original[!missingrows,]

cat("\n\n\n\n\n\n Checking possible control variables: Encounter duration and number of observers
\n\n\n\n\n\n")

#Model with duration as a fixed factor
res_cv=glmer(winner_analysis ~
            durationIGE+num_obs+
            (1|dyad), family="binomial", data=factors_original)

print(summary(res_cv))

#Comparison between the null model and the model with duration as a fixed factor
res.null=glmer(winner_analysis ~ 1 +(1|dyad), family="binomial", data=factors_original)
print(summary(res.null))

print(anova(res.null,res_cv, test="Chisq"))

#Starting a list to calculate AICs to compare between all the models
models<-list()
models[[1]]<-res.null
Modnames <- "Null model"

#Calculating R2
r2_null<-r.squaredGLMM(res.null)

R2<-r2_null
```

```
#Starting another list to calculate AICs to compare between all the models including the one with only relative
use of space as fixed factor
models2<-list()
models2[[1]]<-res.null
Modnames2 <- "Null model"
```

```
#Calculating R2
r2_null2<-r.squaredGLMM(res.null)

R2_2<-r2_null2
```

```
#There is no significant relationships between the potential control variables "durationIGE" and whether the
focal
#group wins an encounter. Thus, they will not be used as a control variable in these analyses
```

```
cat("\n\n\n\n\n Group size and Use of space models \n\n\n\n\n")
```

```
cat("\n\n\n Does group size combined with use of space affects the chances of winning an encounter?\n\n\n")
```

```
# Response: winner_analysis (binary,1=Focal group wins, 0= Focal group loses)
# Fixed effects: rel_groupsize (Number of adult individuals at the Focal Group- Number of adult individuals at
the
# opponent group) and rel_UD190 (Usage of space of G1 on the starting point of the encounter-
# Usage of space G2 on the starting point of the encounter. Usage of space was calculate with BBMM in R,
# with cell.size 190. The BBMM where calculated by calendar month and the values were taken from the
calendar
# month previous to the IGE (e.g. if the encounter was in May, the use of space is the one of April)
#Random effect: 'dyad', 2 levels.
#Hypothesis: The probability of winning an encounter varies with the relative size of the group
#with the group with bigger size more likely to win the encounter (i.e.in this particular data set,
#greater positive rel_groupsize) and the group that uses the area more, more likely to win.
```

```
#Checking colinearity (close to 1 is good, over 4 is a problem)
vif(glm(winner_analysis ~ rel_groupsize+ rel_UD190, family="binomial", data=factors_original))
```

```
#Group size & Relative UD Model(with interactions)
res_gsud=glmer(winner_analysis ~
  rel_groupsize+
  rel_UD190+ rel_groupsize*rel_UD190+
  (1|dyad), family="binomial", data=factors_original)
```

```
print(summary(res_gsud))
```

```
#Group size & Relative UD Model(no interactions)
res_gsud2=glmer(winner_analysis ~
  rel_groupsize+
  rel_UD190+
```

```
(1|dyad), family="binomial", data=factors_original)

print(summary(res_gsud2))

cat("\n\n Comparison of Group size & Relative UD model to null model\n\n")
print(anova(res.null,res_gsud, test="Chisq"))

#Calculate AICs to compare between all the models
models[[2]]<-res_gsud
Modnames <- rbind(Modnames, "Group size and use of space model (interaction)")

#Calculating R2
r2_gsud<-r.squaredGLMM(res_gsud)

R2<-rbind(R2,r2_gsud)

#Calculate AICs to compare between all the models
models2[[2]]<-res_gsud
Modnames2 <- rbind(Modnames2, "Group size and use of space model")

#Calculating R2
r2_gsud<-r.squaredGLMM(res_gsud)

R2_2<-rbind(R2_2,r2_gsud)

#Probability plot
plotLMER.fnc(res_gsud,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of Winning")

cat("\n\n Post-Hoc examination of relative use of space\n\n")

##Separating the 2 dyads to explore differences in slopes (i.e. effects on use of space in winning depending on
dyad)
pb1r1<-(factors_original[factors_original$dyad=="pb1r1",])
res.null_pb1r1=glm(winner_analysis ~ 1 , family="binomial", data=pb1r1)
r1r2<-(factors_original[factors_original$dyad=="r1r2",])
res.null_r1r2=glm(winner_analysis ~ 1 , family="binomial", data=r1r2)

res_pb1r1=glm(winner_analysis ~ rel_groupsize+rel_UD190+rel_groupsize*rel_UD190, family="binomial",
data=pb1r1)
print(summary(res_pb1r1))

sjp.glm(res_pb1r1, type="pred", facet.grid=FALSE, vars="rel_UD190",
        geom.colors = "bw",show.ci=TRUE)
sjp.glm(res_pb1r1, type="pred", facet.grid=FALSE, vars="rel_groupsize",
```

```
geom.colors = "bw",show.ci=TRUE)

str(pb1r1$rel_groupsize)

nooutlier_pb1r1<-pb1r1[pb1r1$rel_groupsize!=10.00,]
str(nooutlier_pb1r1$rel_groupsize)

res_gs2pb1r1=glm(winner_analysis ~ rel_groupsize , family="binomial", data=nooutlier_pb1r1)
print(summary(res_gs2pb1r1))

sjp.glm(res_gs2pb1r1, type="pred", facet.grid=FALSE, vars="rel_groupsize",
        geom.colors = "bw",show.ci=TRUE)

#Apparently the bigger group (r1) has more chances to win (rel_group size is positive) but the larger the
difference, the less chances it has...

cat("\n\n Comparison of Group size & Relative UD (pb1r1) model to null model\n\n")
print(anova(res.null_pb1r1,res_pb1r1, test="Chisq"))


res_r1r2=glm(winner_analysis ~ rel_groupsize+rel_UD190+rel_groupsize*rel_UD190, family="binomial",
data=r1r2)
print(summary(res_r1r2))

cat("\n\n Comparison of Group size & Relative UD (pb1r1) model to null model\n\n")
print(anova(res.null_r1r2,res_r1r2, test="Chisq"))

sjp.glm(res_r1r2, type="pred", facet.grid=FALSE, vars="rel_UD190",
        geom.colors = "bw",show.ci=TRUE)

sjp.glm(res_r1r2, type="pred", facet.grid=FALSE, vars="rel_groupsize",
        geom.colors = "bw",show.ci=TRUE)


cat("\n\n\n\n\n Group size and distance to core area models \n\n\n\n\n")


cat("\n\n\n Does group size combined with distance to core area  the chances of winning an encounter?\n\n\n")

# Response: winner_analysis (binary,1=Focal group wins, 0= Focal group loses)
# Fixed effects: rel_groupsize (Number of adult individuals at the Focal Group- Number of adult individuals at
the
#opponent group) and rel_distancetocorearea (Usage of space of G1 on the starting point of the encounter-
# Usage of space G2 on the starting point of the encounter. Usage of space was calculate with BBMM in R,
# with cell.size 190. The BBMM where calculated by calendar month and the values were taken from the
calendar
# month previous to the IGE (e.g. if the encounter was in May, the use of space is the one of April)
#Random effect: 'dyad', 2 levels.
#Hypothesis: The probability of winning an encounter varies with the relative size of the group
#with the group with bigger size more likely to win the encounter (i.e.in this particular data set,
#greater positive rel_groupsize) and the group that is closer to its core area, more likely to win.

#Checking colinearity (close to 1 is good, over 4 is a problem)
```



```
vif(glm(winner_analysis ~ rel_groupsize+ rel_distancetocorearea, family="binomial", data=factors_original))
```

```
#Group size & Relative distance to core area Model
res_gsdis=glmer(winner_analysis ~
  rel_groupsize+
  rel_distancetocorearea+rel_groupsize*rel_distancetocorearea+
  (1|dyad), family="binomial", data=factors_original)

print(summary(res_gsdis))
```

```
cat("\n\n\n Comparison of Group size & Relative distance to core area model to null model\n\n")
print(anova(res.null,res_gsdis, test="Chisq"))
```

```
#Including results in AIC list
models[[3]]<-res_gsdis
Modnames <- rbind(Modnames, "Group size and distance to core area model")
```

```
#Calculating R2
r2_gsdis<-r.squaredGLMM(res_gsdis)

R2<-rbind(R2,r2_gsdis)
```

```
#Including results in AIC list
models2[[4]]<-res_gsdis
Modnames2 <- rbind(Modnames2, "Group size and distance to core area model")
```

```
#Calculating R2
r2_gsdis<-r.squaredGLMM(res_gsdis)

R2_2<-rbind(R2_2,r2_gsdis)
```

```
#Probability plot
plotLMER.fnc(res_gsdis,ylimit=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="Relative group size",
  ylabel="Probability of Winning")
```

```
cat("\n\n\n Post-hoc exploration of tendencies within each dyad in the effect of distance to core area
differences\n\n")
```

```
#Pb1-r1
res_dpb1r1=glm(winner_analysis ~ rel_distancetocorearea , family="binomial", data=pb1r1)
print(summary(res_dpb1r1))
```

```
sjp.glm(res_dpb1r1, type="pred", facet.grid=FALSE, vars="rel_distancetocorearea",
  geom.colors = "bw",show.ci=TRUE)
```

```
#R1-R2
res_dr1r2=glm(winner_analysis ~ rel_distancetocorearea , family="binomial", data=r1r2)
print(summary(res_dpb1r1))

sjp.glm(res_dr1r2, type="pred", facet.grid=FALSE, vars="rel_distancetocorearea",
        geom.colors = "bw",show.ci=TRUE)

#####

cat("\n\n\n\n\n RESULTS\n\n\n\n\n")

#####
cat("\n\n\nFollowing the regular method \n\n")

## Best model according to AIC

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)

## Best model according to R2

R2

cat("\n\n\n GRAPHS \n\n")

#Groups size+ UD190

sjp.glmer(res_gsud, type="pred", facet.grid=FALSE, vars="rel_groupsize",
        geom.colors = "bw",show.ci=TRUE)

sjp.glmer(res_gsud, type="pred", facet.grid=FALSE, vars="rel_UD190",
        geom.colors = "bw",show.ci=TRUE)

#Groups size+ distance to core

sjp.glmer(res_gsdis, type="pred", facet.grid=FALSE, vars="rel_groupsize",
        geom.colors = "bw",show.ci=TRUE)

sjp.glmer(res_gsdis, type="pred", facet.grid=FALSE, vars="rel_distancetocorearea",
        geom.colors = "bw",show.ci=TRUE)

cat("\n\n\n\n Is there a significant difference in the use of space of the areas where IGEs happen? \n\n")
#PB1-R1 show the expected pattern on how group size and location affect the outcome of encounters, but R1-
R2 does not. I wonder whether having R2 a
```

#smaller homerange, they might be able to overall use more often all parts of their homerange, pushing them to have greater realized RHP in each encounter
 # as opposed to R1, whose home range is bigger and is not normally covered within a days as R2's seemed to be

```
str(factors_original)
```

```
#R1 frequency of use of sites where the analyzed IGEs started
r1_g1<-(factors_original[factors_original$group1=="r1",])
r1_g1_ud<-r1_g1$UD190_g1
r1_g2<-(factors_original[factors_original$group2=="r1",])
r1_g2_ud<-r1_g2$UD190_g2
```

```
r1_ud<-c(r1_g1_ud,r1_g2_ud)
```

```
summary(r1_ud)#Total UD190 for R1
hist(r1_ud)
summary(r1_g1_ud)#IGEs with r2
hist(r1_g1_ud)
summary(r1_g2_ud)#IGEs with pb1
hist(r1_g2_ud)
```

```
#R2 frequency of use of sites where the analyzed IGEs started
r2_g2<-(factors_original[factors_original$group2=="r2",])#In the data base r2 is always g2
summary(r2_g2$UD190_g2)
hist(r2_g2$UD190_g2)
r2_g2_ud<-r2_g2$UD190_g2
```

```
#PB1 frequency of use of sites where the analyzed IGEs started
pb1_g1<-(factors_original[factors_original$group1=="pb1",])#In the data base pb1 is always g1
summary(pb1_g1$UD190_g1)
hist(pb1_g1$UD190_g1)
pb1_g1_ud<-pb1_g1$UD190_g1
```

```
#Wilcoxon paired test
wilcox.test(pb1_g1_ud,r1_g2_ud,conf.int=TRUE,Paired=TRUE)
wilcox.test(r1_g1_ud,r2_g2_ud, conf.int=TRUE,Paired=TRUE)
```

UD190_bygroup<-read.csv("data_UD190onIGEllocations_bygroup.csv")#It was quicker for me to do a data base on excell manually, i'm still not that fluent in R (arg!)

```
ggplot(UD190_bygroup, aes(x=group,y=ud))+
  geom_boxplot()+
  facet_wrap(~dyad)+
  xlab("Group")+
  ylab("IGE area Intensity of Use (%)")
```

#Again pb1-r1 are significantly different (with pb1 often closer to their core areas than r1).
 #R2 shows the same tendency with r1, but is not significant

```
cat("\n\n\n What about home ranges? Does R2 has an higher percentage of core area that might explain higher participation? \n\n")
```

```
homeranges<-read.csv("homeranges_monthlyarea.csv")
hr_nor2<-homeranges[homeranges$Group!="r2",]
hr_nopb1<-homeranges[homeranges$Group!="pb1",]
homeranges$month <- factor(homeranges$month,
levels=c("oct","nov","dec","jan","feb","mar","apr","may","jun"),ordered=TRUE)
```

```
str(homeranges)
```

```
#Home range size and group
```

```
hist(homeranges$hrarea_UD95)
shapiro.test(homeranges$hrarea_UD95)
```

```
anova(lm(hrarea_UD95~Group,data=homeranges))
```

```
ggplot(data=homeranges, aes(x=month, y=hrarea_UD95,group=Group)) +
  geom_line (aes(color=Group))+
  geom_point(aes(color=Group))
```

```
ggplot(homeranges, aes(x=Group,y=hrarea_UD95))+
  geom_boxplot()
```

```
#Core area size and group
```

```
hist(homeranges$core)
shapiro.test(homeranges$core)
```

```
anova(lm(core~Group,data=homeranges))
```

```
ggplot(homeranges, aes(x=Group,y=core))+
  geom_boxplot()
```

```
ggplot(data=homeranges, aes(x=month, y=core,group=Group)) +
  geom_line (aes(color=Group))+
  geom_point(aes(color=Group))
```

```
#Ratio core:hr and group
```

```
hist(homeranges$ratio)
shapiro.test(homeranges$ratio)
```

```
anova(lm(ratio~Group,data=homeranges))
```

```
ggplot(homeranges, aes(x=Group,y=ratio))+
  geom_boxplot()
```

```
ggplot(data=homeranges, aes(x=month, y=ratio,group=Group)) +
  geom_line (aes(color=Group))+
  geom_point(aes(color=Group))+
  xlab("Month")+
  ylab("Core area:Home range area")
```

```
anova(lm(ratio~Group,data=hr_nor2))
```

```
anova(lm(ratio~Group,data=hr_nopb1))
```

2.3.3. MODELS PREDICTING THE PROBABILITY OF AGGRESSIVE ENCOUNTER

```
## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr

# using the package:
updateR() # this will start the updating process of your R installation. It will check for newer versions, and if one
is available, will guide you through the decisions you'd need to make.
```

```
## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine
```

```
library(lme4)
library(car)
library(ggplot2)
library(modEvA)
library(languageR)
library(AICcmodavg)
library(MuMIn)
library(sjPlot)
library(dplyr)
```

```
#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()
```

cat("\n\n\n\n\n\n\n AGGRESSIVE VS NON-AGGRESSIVE ENCOUNTERS\n\n\n\n\n\n\n")

```
## Upload data
factors_original<-read.csv("factors_originalv1.csv")

####Convert variables to the appropriate format
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$aggression_yn <- factor(factors_original$aggression_yn)
factors_original$abs_groupsize<- as.numeric(factors_original$abs_groupsize)
factors_original$abs_UD190<- as.numeric(factors_original$abs_UD190)
factors_original$quartile_UD <- factor(factors_original$quartile_UD)
factors_original$excl_quartilesUD <- factor(factors_original$excl_quartilesUD)
factors_original$abs_distancetocorearea<- as.numeric(factors_original$abs_distancetocorearea)
factors_original$core_yn <- factor(factors_original$core_yn)
factors_original$quartile_dist <- factor(factors_original$quartile_dist)
factors_original$excl_quartilesDist <- factor(factors_original$excl_quartilesDist)

#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison
cannot be made)
#<<values that are missing only for certain variables change the data set and sample size, depending on which
variable is included in
# any given model. I suggest to remove missing cases before starting model selection>> Mazerolle 2017.

missingrows = is.na(factors_original$abs_groupsize)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$aggression_yn)
factors_original= factors_original[!missingrows,]

cat("\n\n\n Checking if control variables are needed \n\n\n")

resa.null0=glmer(aggression_yn ~ 1 +(1|dyad), family="binomial", data=factors_original)
print(summary(resa.null0))

#AIC values to the list
models<-list()
models[[1]]<-resa.null0
Modnames <- "Empty null model"

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
R2_a<-r.squaredGLMM(resa.null0)

cat("\n\n\n Duration & number of observers \n\n\n")

resa_cv=glmer(aggression_yn ~
              durationIGE+num_obs+
              (1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resa_cv))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resa.null0,resa_cv, test="Chisq"))

plotLMER.fnc(resa_cv,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of Aggressive Encounter")

##only duration seem to be explanatory, so it will be kept and the number of obsverers removed
resa.null=glmer(aggression_yn ~
               durationIGE+
               (1|dyad), family="binomial", data=factors_original)
print(summary(resa.null))

plotLMER.fnc(resa.null,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration of IGE",
             ylabel="Probability of Aggressive Encounter")

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resa.null0,resa.null, test="Chisq"))

#Adding result to AIC list
models[[2]]<-resa.null
Modnames <- rbind(Modnames,"Null model (c.v)")

#Calculating R2
r_null<-(r.squaredGLMM(resa.null))
R2_a<-rbind(R2_a,r_null)

cat("\n\n\n\n Models with UD \n\n\n\n\n")

cat("\n\n\n\n Group size and absolute use of space\n\n\n\n\n")

# Following Roths and Cords 206 p.50 "We predicted that [contest duration and [...] level of aggression would
increase (1) when groups were more similar in
# size, (2) with greater symmetry in frequency of use of the contest site and (3) when the contest site was
similarly central in both groups'home ranges."

#Checking colinearity
vif(glm(aggression_yn ~ abs_UD190 +abs_groupsize+durationIGE,family="binomial", data=factors_original))

#Run the model (with interactions)
resa_gsud0=glmer(aggression_yn ~
               abs_UD190 +
```

```
      abs_groupsize+abs_UD190*abs_groupsize+durationlGE+(1|dyad), family="binomial",
data=factors_original)

print(summary(resa_gsud0))
```

```
cat("\n\n Comparison of absolute UD difference and group size model to null model\n\n")
print(anova(resa.null,resa_gsud0, test="Chisq"))
```

```
#Run the model
resa_gsud=glmer(aggression_yn ~
      abs_UD190 +
      abs_groupsize+durationlGE+(1|dyad), family="binomial", data=factors_original)

print(summary(resa_gsud))
```

```
cat("\n\n Comparison of absolute UD difference and group size model to null model\n\n")
print(anova(resa.null,resa_gsud, test="Chisq"))
```

```
plotLMER.fnc(resa_gsud,ylim=0:1,lockYlim=TRUE,linecolor="red",
      lwd=4,
      ylabel="Probability of Aggressive Encounter")
```

```
#Adding result to AIC list
models[[3]]<-resa_gsud
Modnames <- rbind(Modnames,"Group size & abs_UD190")
```

```
#Calculating R2
r2_gsud<-(r.squaredGLMM(resa_gsud))
R2_a<-rbind(R2_a,r2_gsud)
```

```
cat("\n\n and without ppb1r2? n\n\n")
nopb1r2<-factors_original[factors_original$dyad!="pb1r2",]
```

```
#Run the model
resa_gsud2=glmer(aggression_yn ~
      abs_UD190 +
      abs_groupsize+durationlGE+(1|dyad), family="binomial", data=nopb1r2)

print(summary(resa_gsud2))
```

```
cat("\n\n Comparison of absolute UD difference and group size model to null model\n\n")
resa.null2=glmer(aggression_yn ~ durationlGE+(1|dyad), family="binomial", data=nopb1r2)
print(anova(resa.null2,resa_gsud2, test="Chisq"))
```



```

plotLMER.fnc(resa_gsud2,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of Aggressive Encounter")

#####Use of space by quartiles Quartiles#####

cat("\n\n Group Size & Q1 \n\n")

# Data: first_quartile (1st quartile of sum_UD)
# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables:durationIGE
# Fixed effect: abs_UD190 (UD190_G1- UD190_G2) and abs_group size
# Random effect: 'dyad', 2 levels (no IGEs pb1r2 in this quartile)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was low (25% lowest of the
sample), so when both groups had a
# low use of the area, it would be expected that the higher abs_UD190, the lower the probability of aggression
# Then, the lower the differences in group size, the more likely to be aggressive
first_quartile<-factors_original[factors_original$quartile_UD=="1",]
summary(first_quartile$dyad)

#Checking colinearity
vif(glm(aggression_yn ~ abs_UD190 +abs_groupsize+durationIGE,family="binomial", data=first_quartile))

#Run the model
resa_qud1gs0=glmer(aggression_yn ~
                  abs_UD190 +
                  abs_groupsize+abs_UD190*abs_groupsize+durationIGE+(1|dyad), family="binomial",
                  data=first_quartile)

print(summary(resa_qud1gs0))

#Run the model
resa_qud1gs=glmer(aggression_yn ~
                  abs_UD190 +
                  abs_groupsize+durationIGE+(1|dyad), family="binomial", data=first_quartile)

print(summary(resa_qud1gs))

cat("\n\n Comparison of 1st quartile & group size model to null model\n\n")
resa.null1q<-glmer(aggression_yn ~ durationIGE+(1|dyad),family="binomial", data=first_quartile)
print(anova(resa.null1q,resa_qud1gs, test="Chisq"))

plotLMER.fnc(resa_qud1gs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Groups size and 1Q UD",
             ylabel="Probability of Aggressive Encounter-1st quartile")

# Data: third_quartile 3rd quartile of sum_UD

```

```

# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables: durationIGE (Separated, see below)
# Fixed effect: abs_UD190 (UD190_G1- UD190_G2)
# Random effect: 'dyad', 2 levels (pb1r2 has no IGE in this quartile)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was high (25% highest of the
sample), it would be expected that
# the probability of aggression is comparatively higher than in the first case and would increase the more similar
the use of space is )
# the lower the abs_UD190)
third_quartile<-factors_original[factors_original$quartile_UD=="3",]
summary(third_quartile$dyad)

#Checking colinearity
vif(glm(aggression_yn ~ abs_UD190 +abs_groupsize+durationIGE,family="binomial", data=third_quartile))

#Model
resa_qud3gs0=glmer(aggression_yn ~
  abs_groupsize+abs_UD190+abs_groupsize*abs_UD190+durationIGE+
  (1|dyad), family="binomial", data=third_quartile)

print(summary(resa_qud3gs0))

#Model
resa_qud3gs=glmer(aggression_yn ~
  abs_groupsize+abs_UD190+durationIGE+
  (1|dyad), family="binomial", data=third_quartile)

print(summary(resa_qud3gs))

cat("\n\n\n Comparison of Q3 sum_UD model & group size model to null model\n\n")
resa.null3qd<-glmer(aggression_yn ~ durationIGE +(1|dyad),family="binomial", data=third_quartile)
print(anova(resa.null3qd,resa_qud3gs, test="Chisq"))

plotLMER.fnc(resa_qud3gs,ylim=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="abs(relative use)",
  ylabel="Probability of Aggressive Encounter-3rd quartile")

#####Low VS High use of Space#####

# Data: low_absUD_quartiles
# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE) # Control variables: num_obs and
durationIGE
# Fixed effect: quartile_UD (categorical) and abs_groupsize
# Random effect: 'dyad', 2 levels (pb1r2 has no IGE in this quartile)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was high (25% highest of the
sample) or low(25% lowest of the sample) ,
# and where differences in usage between the groups are low (only the lowest third of data of abs_UD190 were
selected), we would expect Q1 to have a

```

```
# significantly lower probability of Aggressive Encounter than the Q3. Then, the lower the difference is group
size, the higher the probability of
# aggression
quartiles1and3<-factors_original[factors_original$quartile_UD!="2",] #Take only the 1st and 3rd quartiles of
sum_UD
low_absUD_quartiles<-quartiles1and3[quartiles1and3$excl_quartilesUD=="1",] #From the previous result, take
only the ones with low abs_UD
resa.nullq<-glmer(aggression_yn ~ durationIGE+(1|dyad),family="binomial", data=low_absUD_quartiles)

vif(glm(aggression_yn ~ quartile_UD +abs_groupsize+durationIGE, family="binomial",
data=low_absUD_quartiles))

#Run the model quartiles (with interactions)
resa_udqgs0=glmer(aggression_yn ~
  quartile_UD +
  abs_groupsize+quartile_UD*abs_groupsize+
  durationIGE+
  (1|dyad), family="binomial", data=low_absUD_quartiles)

print(summary(resa_udqgs0))

#Run the model quartiles
resa_udqgs=glmer(aggression_yn ~
  quartile_UD +
  abs_groupsize+
  durationIGE+
  (1|dyad), family="binomial", data=low_absUD_quartiles)

print(summary(resa_udqgs))

cat("\n\n\n Comparison of Qs Sum_UD & Group size model to null model\n\n")

print(anova(resa.nullq,resa_udqgs, test="Chisq"))

plotLMER.fnc(resa_udqgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="Quartiles",
  ylabel="Probability of Aggressive Encounter")

cat("\n\n\n\n Models with core area \n\n\n\n")

cat("\n\n\n\n\n Group size and absolute distance to core area\n\n\n\n\n")
#Following predictions similar to Roths & Cords 2016

#Checking colinearity
vif(glm(aggression_yn ~ abs_groupsize+abs_distancetocorearea+durationIGE,family="binomial",
data=factors_original))
```

```

#Run the model (with interactions)
resa_gsds=glmer(aggression_yn ~
  abs_groupsize+abs_distancetocorearea+abs_groupsize*abs_distancetocorearea+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resa_gsds))

cat("\n\n Comparison of Group size and absolute distance to core area Model to null model\n\n")
print(anova(resa.null,resa_gsds, test="Chisq"))

#Run the model
resa_gsds=glmer(aggression_yn ~
  abs_groupsize+abs_distancetocorearea+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resa_gsds))

cat("\n\n Comparison of Group size and absolute distance to core area Model to null model\n\n")
print(anova(resa.null,resa_gsds, test="Chisq"))

plotLMER.fnc(resa_gsds,ylimit=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,
  ylabel="Probability of Aggressive Encounter")

#Adding result to AIC list
models[[4]]<-resa_gsds
Modnames <- rbind(Modnames,"Group size & abs_distance to core")

#Calculating R2
r2_gsds<-(r.squaredGLMM(resa_gsds))
R2_a<-rbind(R2_a,r2_gsds)

cat("\n\n\n\n Group size & Categorical core area\n\n\n\n")

# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables: durationIGE
# Fixed effect: core_yn (y=1 group was in its core area, n= no group was in its core area, b=both groups were in
a core area) and abs_groupsize
# Random effect: 'dyad', 3 levels.
# Hypothesis: Encounters will be more likely to be aggressive when both groups are in their core area and lower
when none is. Also, the more
# similar the group sizes, the more likely the encounter would be aggressive

#Checking colinearity
vif(glm(aggression_yn ~ core_yn+abs_groupsize+durationIGE,family="binomial", data=factors_original))

#Run the model(with interactuons)
resa_cyngs0=glmer(aggression_yn ~
  core_yn +
  abs_groupsize+core_yn*abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resa_cyngs0))

```

```
cat("\n\n Comparison of Group size and absolute distance to core area Model to null model\n\n")
print(anova(resa.null,resa_cyngs0, test="Chisq"))

#Run the model
resa_cyngs=glmer(aggression_yn ~
  core_yn +
  abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resa_cyngs))

cat("\n\n Comparison of Group size and absolute distance to core area Model to null model\n\n")
print(anova(resa.null,resa_cyngs, test="Chisq"))

plotLMER.fnc(resa_cyngs,ylimit=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="Core area y/n & group size Model",
  ylabel="Probability of Aggressive Encounter")

#Adding result to AIC list
models[[5]]<-resa_cyngs
Modnames <- rbind(Modnames,"Group size & categorical core area")

#Calculating R2
r2_cyngs<-(r.squaredGLMM(resa_cyngs))
R2_a<-rbind(R2_a,r2_cyngs)

table(factors_original$core_yn,
  factors_original$aggression_yn)

###To explore why this model explains 91% variance and has an S.E so high, i'll try to see what happens when I
eliminate the 5 cases in which both
# groups were in the core area (always aggressive), which according to the sjPlot might be biasing the results
nob<-factors_original[factors_original$core_yn!="b",]

resa_cyngs2=glmer(aggression_yn ~
  core_yn +
  abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=nob)

print(summary(resa_cyngs2))

r.squaredGLMM(resa_cyngs2)

#Once the 5 encounters that started in locations that were core areas for both groups are removed, then the SE
and the R2 drop to levels of the other models
```

```
cat("\n\n\n\n Distance to core area by quartiles & Group size \n\n\n\n\n")
```

```
# Data: first_quartile dis (1st quartile of sum_distancetocorearea)
# Response: aggression_yn (binary, 1= Aggressive IGE, 0= Non-aggressive IGE)
# Fixed effect: abs_distancetocorearea (abs(distancetocorearea_G1- distancetocorearea_G2)) + abs_groupsize
# Control variables: duration_IGE
# Random effect: 'dyad', 2 levels, no IGEs pb1r2 in this category
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was low (25%
lowest of the sample), so when
# both groups were close to their core area, it would be expected that the lower the abs_UD190, the higher the
probability of a aggressive encounter
# since both are expected to value highly the resources around and to fight for them until one is displaced. The
more similar the group
# size, the more likely the aggression
first_quartiledis<-factors_original[factors_original$quartile_dist=="1",]
summary(first_quartile$dyad)
resa.null1qdis<-glmer(aggression_yn ~ durationIGE +(1|dyad),family="binomial", data=first_quartiledis)
```

```
#Checking colinearity
vif(glm(aggression_yn ~ abs_distancetocorearea+abs_groupsize+durationIGE,family="binomial",
data=first_quartiledis))
```

```
#Run the model (with interactions)
resa_q1disgs0=glmer(aggression_yn ~
abs_distancetocorearea+abs_groupsize+abs_distancetocorearea*abs_groupsize+durationIGE
+(1|dyad), family="binomial", data=first_quartiledis)
```

```
print(summary(resa_q1disgs0))
```

```
#Run the model
resa_q1disgs=glmer(aggression_yn ~
abs_distancetocorearea+abs_groupsize+durationIGE +(1|dyad), family="binomial",
data=first_quartiledis)
```

```
print(summary(resa_q1disgs))
```

```
cat("\n\n\n Comparison of Q1 sum_distancetocorearea & group size model to null model\n\n")
```

```
print(anova(resa.null1qdis,resa_q1disgs, test="Chisq"))
```

```
plotLMER.fnc(resa_q1disgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,xlabel="abs(relative distance to core area)",
ylabel="Probability of aggressive encounter-1st quartile")
```

```
# Data: third_quartile 3rd quartile of sum_distancetocorearea
# Response: aggression_yn (binary, 1= Aggressive IGE, 0= Non-aggressive IGE)
# Fixed effect: abs_distancetocorearea (abs(distancetocorearea_G1- distancetocorearea_G2))+abs_groupsize
# Control variables: duration_IGE
# Random effect: 'dyad', 3 levels.
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was high (25%
highest of the sample), it would be
# expected that the higher the difference (i.e. abs_distancetocorearea), the lower the probabilities of an
aggressive encounter
```

```

# (one would have more reasons to fight and the other to withdraw)
third_quartiledis<-factors_original[factors_original$quartile_dist=="3",]
resa.null3qdis<-glmer(aggression_yn ~ durationIGE+(1|dyad),family="binomial", data=third_quartiledis)

#Checking colinearity
vif(glm(aggression_yn ~ abs_distancetocorearea+abs_groupsize+durationIGE,family="binomial",
data=third_quartiledis))

#Run the model(with interactions)
resa_q3disgs0=glmer(aggression_yn ~
                    abs_distancetocorearea +abs_groupsize+abs_distancetocorearea*abs_groupsize+durationIGE+
                    (1|dyad), family="binomial", data=third_quartiledis)

print(summary(resa_q3disgs0))

#Run the model
resa_q3disgs=glmer(aggression_yn ~
                    abs_distancetocorearea +abs_groupsize+durationIGE+
                    (1|dyad), family="binomial", data=third_quartiledis)

print(summary(resa_q3disgs))

cat("\n\n\n Comparison of Q3 sum_dis+group size model to null model\n\n")

print(anova(resa.null3qdis,resa_q3disgs, test="Chisq"))

plotLMER.fnc(resa_q3disgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="abs(relative distance to core area)",
             ylabel="Probability of aggressive encounter-3rd quartile")

cat("\n\n\n\n\n Close to Core VS Far From Core\n\n\n\n")

# Data: quartiles_dist
# Response: aggression_yn (binary,1= Aggressive IGE, 0= Non-aggressive IGE)
# Fixed effect: quartiles of distance to core area (1 with low sum and another with high sum) +abs_groupsize
# Control variables: duration_IGE
# Random effect: 'dyad', 3 levels.
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was high (25%
highest of the sample) or
# low(25% lowest of the sample) we would expect Q1 to have a significantly higher probability of aggressive
encounter than the Q3. Then, the more
# similar the group sizes, the more likely the aggression.
quartiles_dist<-factors_original[factors_original$excl_quartilesDist=="1",] #Takes the Q1 and Q3 of
sum_distancetocorearea
resa.nullqdis<-glmer(aggression_yn ~ durationIGE +(1|dyad),family="binomial", data=quartiles_dist)

#Checking colinearity
vif(glm(aggression_yn ~ abs_distancetocorearea+abs_groupsize+durationIGE,family="binomial",
data=quartiles_dist))

```

```

#Run the model quartiles (with interactions)
resa_disqgs0=glmer(aggression_yn ~
  quartile_dist+abs_groupsize+quartile_dist*abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=quartiles_dist)

print(summary(resa_disqgs0))

#Run the model quartiles
resa_disqgs=glmer(aggression_yn ~
  quartile_dist+abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=quartiles_dist)

print(summary(resa_disqgs))

cat("\n\n\n Comparison of Qs sum_dis + group size model to null model\n\n")

print(anova(resa.nullqdis,resa_disqgs, test="Chisq"))

plotLMER.fnc(resa_disqgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="Quartiles distance",
  ylabel="Probability of aggressive encounter")

#####
#####
#####
#####
cat("\n\n\n SUMMARY OF RESULTS\n\n")
#####
#####
#####
#####
aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_a

##The only significant variable was duration. The model with it was significantly different from the null and
seems to explain 50% of the
# variability (mostly fixed factor, no effect of random)

sjp.glmer(resa.null, type="pred", facet.grid=FALSE, vars="durationIGE",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resa_gsud, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resa_gsud, type="pred", facet.grid=FALSE, vars="abs_UD190",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resa_gsds, type="pred", facet.grid=FALSE, vars="abs_distancetocorearea",
  geom.colors = "bw",show.ci=TRUE)

```

```
sjp.glmer(resa_cyngs, type="pred", facet.grid=FALSE, vars="core_yn",
  geom.colors = "bw",show.ci=TRUE)
```

```
#What variability does dyad explain?
```

```
table(factors_original$aggression_yn,
  factors_original$dyad)
```

```
cat("\n\n\n\n What is the relationship between decided-undecided encounters and aggression?\n\n\n")
```

```
#0=IGE without aggression; 1=Aggressive IGE
ggplot(factors_original, aes(x=decided_undecided, fill=aggression_yn))+
  geom_bar(position="fill")+
  ylab("proportion")
```

```
Table<-table(factors_original$aggression_yn,
  factors_original$decided_undecided)
rownames(Table)<-c("Non-aggressive","Aggressive")
colnames(Table)<-c("Undecided","Decided")
Table
```

```
pb1r1<-(factors_original[factors_original$dyad=="pb1r1",])
Table_pb1r1<-table(pb1r1$aggression_yn,
  pb1r1$decided_undecided)
rownames(Table_pb1r1)<-c("Non-aggressive","Aggressive")
colnames(Table_pb1r1)<-c("Undecided","Decided")
```

```
r1r2<-(factors_original[factors_original$dyad=="r1r2",])
Table_r1r2<-table(r1r2$aggression_yn,
  r1r2$decided_undecided)
rownames(Table_r1r2)<-c("Non-aggressive","Aggressive")
colnames(Table_r1r2)<-c("Undecided","Decided")
```

```
pb1r2<-(factors_original[factors_original$dyad=="pb1r2",])
```

```
Table_pb1r2<-table(pb1r2$aggression_yn,
  pb1r2$decided_undecided)
rownames(Table_pb1r2)<-c("Non-aggressive","Aggressive")
colnames(Table_pb1r2)<-c("Undecided")
```

```
Table_pb1r1
Table_r1r2
Table_pb1r2
```

```
chisq.test(Table_pb1r1)
chisq.test(Table_r1r2)
#There is no reason to believe that outcome (decided vs draw) and presence/absence of aggression are related
```

2.3.4. MODELS PREDICTING THE PROBABILITY OF PRESENCE OF CONTACT AGGRESSION IN AGGRESSIVE ENCOUNTERS

```
## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr

# using the package:
updateR() # this will start the updating process of your R installation. It will check for newer versions, and if one
is available, will guide you through the decisions you'd need to make.

## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the fata points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine

library(lme4)
library(car)
library(ggplot2)
library(modEvA)
library(languageR)
library(AICcmodavg)
library(MuMIn)
library(sjPlot)
library(dplyr)

#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()
```



```
#Comparison between the null model and the model with the potential c.v
print(anova(resal.null0,resal_cv, test="Chisq"))

plotLMER.fnc(resal_cv,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of Highly aggressive Encounter")

#Only the duration is significant. Therefore, will be the only control variable kept

#Null model (with c.v.)
resal.null=glmer(aggression_level ~
                durationIGE+
                (1|dyad), family="binomial", data=factors_original)

print(summary(resal.null))

#Comparison between the null model and the model with the potential c.v
print(anova(resal.null0,resal.null, test="Chisq"))

#Adding result to AIC list
models[[2]]<-resal.null
Modnames <- rbind(Modnames,"Null model (c.v)")

#Calculating R2
r_null<-(r.squaredGLMM(resal.null))
R2_al<-rbind(R2_al,r_null)

plotLMER.fnc(resal.null,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration of IGE",
             ylabel="Probability of Highly aggressive Encounter")

cat("\n\n\n\n Models with UD \n\n\n\n\n")

cat("\n\n\n\n Group size and absolute use of space\n\n\n\n\n")

# Following Roths and Cords 206 p.50 "We predicted that [contest duration and [...] level of aggression would
increase (1) when groups were more similar in
# size, (2) with greater symmetry in frequency of use of the contest site and (3) when the contest site was
similarly central in both groups'home ranges."

#Checking colinearity
vif(glm(aggression_level ~ abs_UD190 +abs_groupsize+durationIGE,family="binomial", data=factors_original))

#Run the model(with interactions)
resal_gsud0=glmer(aggression_level ~
                abs_UD190 +
```

```
      abs_groupsize+abs_UD190*abs_groupsize+durationIGE+(1|dyad), family="binomial",
data=factors_original)

print(summary(resal_gsud0))
```

```
cat("\n\n\n Comparison of absolute UD difference and group size model to null model\n\n")
print(anova(resal.null,resal_gsud0, test="Chisq"))
```

```
#Run the model
resal_gsud=glmer(aggression_level ~
      abs_UD190 +
      abs_groupsize+durationIGE+(1|dyad), family="binomial", data=factors_original)

print(summary(resal_gsud))
```

```
cat("\n\n\n Comparison of absolute UD difference and group size model to null model\n\n")
print(anova(resal.null,resal_gsud, test="Chisq"))
```

```
plotLMER.fnc(resal_gsud,ylim=0:1,lockYlim=TRUE,linecolor="red",
      lwd=4,xlabel="Groups size and 1Q UD",
      ylabel="Probability of Highly Aggressive Encounter")
```

```
#Adding result to AIC list
models[[3]]<-resal_gsud
Modnames <- rbind(Modnames,"Group size & abs_UD190")
```

```
#Calculating R2
r2_gsud<-(r.squaredGLMM(resal_gsud))
R2_al<-rbind(R2_al,r2_gsud)
```

##Group size and duration were significant. A new model is created keeping these two variables

```
#Run the model
resal_gs=glmer(aggression_level ~
      abs_groupsize+durationIGE+(1|dyad), family="binomial", data=factors_original)

print(summary(resal_gs))
```

```
cat("\n\n\n Comparison of absolute group size model to null model\n\n")
print(anova(resal.null,resal_gs, test="Chisq"))
```

```
plotLMER.fnc(resal_gs,ylim=0:1,lockYlim=TRUE,linecolor="red",
      lwd=4,
      ylabel="Probability of Highly Aggressive Encounter")
```

```
#Adding result to AIC list
```

```

models[[4]]<-resal_gs
Modnames <- rbind(Modnames,"Group size")

#Calculating R2
r2_gs<-(r.squaredGLMM(resal_gs))
R2_al<-rbind(R2_al,r2_gs)

cat("\n\n\n Is this due to the 2 IGE between pb1r2?\n\n")
nopb1r2<-factors_original[factors_original$dyad!="pb1r2",]

resal_gs2=glmer(aggression_level ~
  abs_groupsize+durationIGE+(1|dyad), family="binomial", data=nopb1r2)

print(summary(resal_gs2))

plotLMER.fnc(resal_gs2,ylim=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,
  ylabel="Probability of Highly Aggressive Encounter")

cat("\n\n\n Comparison of absolute group size model to null model\n\n")
resal.null2=glmer(aggression_level ~
  durationIGE+(1|dyad), family="binomial", data=nopb1r2)
print(anova(resal.null2,resal_gs2, test="Chisq"))

cat("\n\n\n Use of space by Quartiles \n\n")

# Data: first_quartile (1st quartile of sum_UD)
# Response: aggression_level (binary,1=contact aggression IGE, 0=Non-contact aggression IGE)
# Control variable: durationIGE
# Fixed effect: abs_UD190 (UD190_G1- UD190_G2) and abs_group size
# Random effect: 'dyad', 2 levels (no IGEs pb1r2 in this quartile)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was low (25% lowest of the
# sample), so when both groups had a
# low use of the area, it would be expected that the higher abs_UD190, the lower the probability of high level
# aggression (but overall should be low)
# Then, the lower the differences in group size, the more likely to be highly aggressive
first_quartile<-factors_original[factors_original$quartile_UD=="1",]
summary(first_quartile$dyad)

#Checking colinearity
vif(glm(aggression_level ~ abs_UD190 +abs_groupsize+durationIGE,family="binomial", data=first_quartile))

#Run the model (with interactions)
resal_qud1gs=glmer(aggression_level ~
  abs_UD190 +abs_groupsize+abs_UD190*abs_groupsize+durationIGE+(1|dyad), family="binomial",
  data=first_quartile)

print(summary(resal_qud1gs))

```

```
cat("\n\n Comparison of Q1 sum_UD & group size model to null model\n\n")
resal.null1q<-glmer(aggression_level ~ durationIGE+(1|dyad),family="binomial", data=first_quartile)
print(anova(resal.null1q,resal_qud1gs, test="Chisq"))

#Run the model (without interactions)
resal_qud1gs=glmer(aggression_level ~
  abs_UD190 +abs_groupsize+durationIGE+(1|dyad), family="binomial", data=first_quartile)

print(summary(resal_qud1gs))

cat("\n\n Comparison of Q1 sum_UD & group size model to null model\n\n")
resal.null1q<-glmer(aggression_level ~ durationIGE+(1|dyad),family="binomial", data=first_quartile)
print(anova(resal.null1q,resal_qud1gs, test="Chisq"))

plotLMER.fnc(resal_qud1gs,ylim=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="Groups size and 1Q UD",
  ylabel="Probability of Highly Aggressive Encounter-1st quartile")

# Data: third_quartile 3rd quartile of sum_UD
# Response: aggression_level (binary,1=Contact aggression IGE, 0=Non-contact aggression IGE)
# Control variable:durationIGE
# Fixed effect: abs_UD190 (UD190_G1- UD190_G2) and abs_groupsize
# Random effect: 'dyad', 2 levels (pb1r2 has no IGE in this quartile)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was high (25% highest of the
sample), it would be expected that
# the probability of high level aggression is comparatively higher than in the first case and would increase the
more similar the use of space is )
# the lower the abs_UD190). The more similar the group size, the more likely the contact aggression

third_quartile<-factors_original[factors_original$quartile_UD=="3",]
summary(third_quartile$dyad)

#Checking colinearity
vif(glm(aggression_level ~ abs_UD190 +abs_groupsize+durationIGE,family="binomial", data=third_quartile))

#Run the model
resal_qud3gs0=glmer(aggression_level ~
  abs_UD190+abs_groupsize+abs_UD190*abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=third_quartile)

print(summary(resal_qud3gs0))

#Run the model
resal_qud3gs=glmer(aggression_level ~
```

```

    abs_UD190+abs_groupsize+durationIGE+
    (1|dyad), family="binomial", data=third_quartile)

print(summary(resal_qud3gs))

cat("\n\n Comparison of Q3 sum_UD+ group size model to null model\n\n")
resal.null3q<-glmer(aggression_level ~ durationIGE +(1|dyad),family="binomial", data=third_quartile)
print(anova(resal.null3q,resal_qud3gs, test="Chisq"))

plotLMER.fnc(resal_qud3gs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="abs(relative use)",
             ylabel="Probability of Highly Aggressive Encounter-3rd quartile")

cat("\n\n Low VS High use \n\n")

# Data: low_absUD_quartiles
# Response: aggression_level (binary,1=Contact aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: quartile_UD (categorical) and abs_groupsize
# Random effect: 'dyad', 2 levels (pb1r2 have no IGEs in these categories)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_UD was high (25% highest of the
sample) or low(25% lowest of the sample) ,
# and where differences in usage between the groups are low (only the lowest third of data of abs_UD190 were
selected), we would expect Q1 to have a
# significantly lower Probability of Highly Aggressive Encounter than the Q3. Then, the lower the difference is
group size, the higher the probability of
# aggression

quartiles1and3<-factors_original[factors_original$quartile_UD!="2",] #Take only the 1st and 3rd quartiles of
sum_UD
low_absUD_quartiles<-quartiles1and3[quartiles1and3$excl_quartilesUD=="1",] #From the previous result, take
only the ones with low abs_UD
resal.nullq<-glmer(aggression_level ~ durationIGE+(1|dyad),family="binomial", data=low_absUD_quartiles)

#Checking colinearity
vif(glm(aggression_yn ~ quartile_UD +abs_groupsize+durationIGE, family="binomial",
data=low_absUD_quartiles))

#Run the model quartiles
resal_udqgs0=glmer(aggression_level ~
    quartile_UD +
    abs_groupsize+ quartile_UD*abs_groupsize+
    durationIGE+
    (1|dyad), family="binomial", data=low_absUD_quartiles)

print(summary(resal_udqgs0))

#Run the model quartiles
resal_udqgs=glmer(aggression_level ~
    quartile_UD +
    abs_groupsize+

```



```
durationIGE+
(1|dyad), family="binomial", data=low_absUD_quartiles)

print(summary(resal_udqgs))

cat("\n\n\n Comparison of Qs sum_UD+group size model to null model\n\n")
print(anova(resal.nullq,resal_udqgs, test="Chisq"))

plotLMER.fnc(resal_udqgs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Quartiles",
             ylabel="Probability of Highly Aggressive Encounter")

cat("\n\n\n\n Models with core area \n\n\n\n\n")

cat("\n\n\n\n Group size and absolute difference in distance to core area \n\n\n\n\n")

# Following Roths and Cords 206 p.50 "We predicted that [contest duration and [...] level of aggression would
increase (1) when groups were more similar in
# size, (2) with greater symmetry in frequency of use of the contest site and (3) when the contest site was
similarly central in both groups'home ranges."

#Checking colinearity
vif(glm(aggression_level ~ abs_groupsize+abs_distancetocorearea +durationIGE,family="binomial",
data=factors_original))

#Run the model(interactions)
resal_gsds0=glmer(aggression_level ~

abs_groupsize+abs_distancetocorearea+abs_groupsize*abs_distancetocorearea+durationIGE+(1|dyad),
family="binomial", data=factors_original)

print(summary(resal_gsds0))

#Run the model
resal_gsds=glmer(aggression_level ~
                abs_groupsize+abs_distancetocorearea+durationIGE+(1|dyad), family="binomial",
data=factors_original)

print(summary(resal_gsds))

cat("\n\n\n\n Comparison of absolute distance to core and group size model to null model\n\n")
print(anova(resal.null,resal_gsds, test="Chisq"))
```

```
plotLMER.fnc(resal_gsds,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of Highly Aggressive Encounter")

#Adding result to AIC list
models[[5]]<-resal_gsds
Modnames <- rbind(Modnames,"Group size & abs_distance")

#Calculating R2
r2_gsds<-(r.squaredGLMM(resal_gsds))
R2_al<-rbind(R2_al,r2_gsds)

#Again, the selected model would be that retaining only absolute difference in group size and duration of
encounter, which is already modeled

cat("\n\n\n Group size and categorical core area\n\n")
# Response: aggression_level (binary,1=Contact aggression IGE, 0=Non-contact aggression IGE)
# Control variable: durationIGE
# Fixed effect: core_yn (y=1 group was in its core area, n= no group was in its core area, b=both groups were in
a core area) and abs_groupsize
# Random effect: 'dyad', 3 levels.
# Hypothesis: Encounters will be more likely to be highly aggressive when both groups are in their core area and
lower when none is. Also, the more
# similar the group sizes, the more likely the encounter would be highly aggressive

#Checking colinearity
vif(glm(aggression_level ~ core_yn+abs_groupsize+durationIGE,family="binomial", data=factors_original))

#Run the model (with interactions)
resal_cyngs0=glmer(aggression_level ~
                  abs_groupsize+durationIGE+core_yn +abs_groupsize*core_yn+
                  (1|dyad), family="binomial", data=factors_original)

print(summary(resal_cyngs0))

#Run the model
resal_cyngs=glmer(aggression_level ~
                  abs_groupsize+durationIGE+core_yn +
                  (1|dyad), family="binomial", data=factors_original)

print(summary(resal_cyngs))

cat("\n\n\n Comparison of Core area y/n & group size Model to null model\n\n")
print(anova(resal.null,resal_cyngs, test="Chisq"))

#Again abs_groupsize and duration are the only significant variables, and a new model only with them was
previously created
```

```
#Adding result to AIC list
models[[6]]<-resal_cyngs
Modnames <- rbind(Modnames,"Group size & categorical core area model")

#Calculating R2
r2_cyngs<-(r.squaredGLMM(resal_cyngs))
R2_al<-rbind(R2_al,r2_cyngs)

plotLMER.fnc(resal_cyngs,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Core area y/n & group size Model",
             ylabel="Probability of Highly Aggressive Encounter")

ggplot(factors_original, aes(x=core_yn, fill=aggression_level),na.rm=TRUE)+
  geom_bar()

cat("\n\n\n\n\n Distance to core area by quartiles & Group size \n\n\n\n\n")

# Data: first_quartile dis (1st quartile of sum_distancetocorearea)
# Response: aggression_level (binary,1=Contact Aggression IGE, 0=Non-contact Aggression IGE)
# Fixed effect: abs_distancetocorearea (abs(distancetocorearea_G1- distancetocorearea_G2)) + abs_groupsize
# Control variable: duration_IGE
# Random effect: 'dyad', 2 levels (pb1r2 have no IGEs in this category)
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was low (25%
lowest of the sample), so when
# both groups were close to their core area, it would be expected that the lower the abs_dist, the higher the
probability of a highly aggressive
# encounter since both are expected to value highly the resources around and to fight for them until one is
displaced. The more similar the group
# size, the more likely the contact aggression
first_quartiledis<-factors_original[factors_original$quartile_dist=="1",]
summary(first_quartile$dyad)
resal.null1qdis<-glmer(aggression_level ~ durationIGE +(1| dyad),family="binomial", data=first_quartiledis)
print(summary(resal.null1qdis))

plotLMER.fnc(resal.null1qdis,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of highly aggressive encounter-1st quartile")

#Starting a list to calculate AICs to compare between all the models
modelsQ1dis<-list()
modelsQ1dis[[1]]<-resal.null1qdis
ModnamesQ1dis <- "Null model Q1dis"

#Calculating R2
r2_nullQ1dis<-r.squaredGLMM(resal.null1qdis)

R2_Q1dis<-r2_nullQ1dis
```

```
#Checking colinearity
vif(glm(aggression_level ~ abs_distancetocorearea+abs_groupsize+durationIGE,family="binomial",
data=first_quartiledis))

#Run the model (with interactions)
resal_q1disgs0=glmer(aggression_level ~
  abs_distancetocorearea+abs_groupsize+abs_distancetocorearea*abs_groupsize+durationIGE
+(1|dyad), family="binomial", data=first_quartiledis)

print(summary(resal_q1disgs0))

#Run the model
resal_q1disgs=glmer(aggression_level ~
  abs_distancetocorearea+abs_groupsize+durationIGE +(1|dyad), family="binomial",
data=first_quartiledis)

print(summary(resal_q1disgs))

cat("\n\n\n Comparison of Q1sum_distancetocorearea + group size model to null model\n\n")
print(anova(resal.null1qdis,resal_q1disgs, test="Chisq"))

#Including model in AIC list
modelsQ1dis[[2]]<-resal_q1disgs
ModnamesQ1dis<-rbind(ModnamesQ1dis, "gs+Q1 dis model")

#Calculating R2

r2_q1dis<-r.squaredGLMM(resal_q1disgs)
R2_Q1dis<-rbind(R2_Q1dis,r2_q1dis)

plotLMER.fnc(resal_q1disgs,ylimit=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,
  ylabel="Probability of highly aggressive encounter-1st quartile")

# Data: third_quartile 3rd quartile of sum_distancetocorearea
# Response: aggression_level (binary,1=Contact Aggression IGE, 0=Non-contact Aggression IGE)
# Fixed effect: abs_distancetocorearea (abs(distancetocorearea_G1- distancetocorearea_G2))+abs_groupsize
# Control variable:duration_IGE
# Random effect: 'dyad', 3 levels.
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was high (25%
highest of the sample), it would be
# expected that the higher the difference (i.e. abs_distancetocorearea), the lower the probabilities of an highly
aggressive encounter
# (one would have more reasons to fight and the other to withdraw) Overall should be low
third_quartiledis<-factors_original[factors_original$quartile_dist=="3",]
resal.null3qdis<-glmer(aggression_level ~ durationIGE+(1|dyad),family="binomial", data=third_quartiledis)
```

```

#Checking colinearity
vif(glm(aggression_level ~ abs_distancetocorearea+abs_groupsize+durationIGE,family="binomial",
data=third_quartiledis))

#Run the model(with interactions)
resal_q3disgs0=glmer(aggression_level ~
  abs_distancetocorearea +abs_groupsize+ abs_distancetocorearea*abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=third_quartiledis)

print(summary(resal_q3disgs0))

#Run the model
resal_q3disgs=glmer(aggression_level ~
  abs_distancetocorearea +abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=third_quartiledis)

print(summary(resal_q3disgs))

cat("\n\n\n Comparison of Q3 sum_dis+group size model to null model\n\n")

print(anova(resal.null3qdis,resal_q3disgs, test="Chisq"))

plotLMER.fnc(resal_q3disgs,ylimit=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="abs(relative distance to core area)",
  ylabel="Probability of highly aggressive encounter-3rd quartile")

cat("\n\n\n\n\n Close to core VS far from core\n\n\n\n")

# Data: quartiles_distancetocore
# Response: aggression_level (binary,1=Contact Aggression IGE, 0=Non-contact Aggression IGE)
# Fixed effect: quartiles of distance to core area (1 with low sum and another with high sum) +abs_groupsize
# Control variable:duration_IGE
# Random effect: 'dyad', 3 levels.
# Hypothesis: Given that we are only analysing those IGEs in which the sum_distancetocorearea was high (25%
highest of the sample) or
# low(25% lowest of the sample) , we would expect Q1 has a significantly higher Probability of Highly Aggressive
Encounter than the Q3. Also,
# the more equal the group sizes (abd_groupsize closer to zero), the more likely the contact aggression
quartiles_dist<-factors_original[factors_original$excl_quartilesDist=="1",] #Takes the Q1 and Q3 of
sum_distancetocorearea
resal.nullqdis<-glmer(aggression_level ~ durationIGE +(1|dyad),family="binomial", data=quartiles_dist)

#Checking colinearity
vif(glm(aggression_level ~ abs_distancetocorearea+abs_groupsize+durationIGE,family="binomial",
data=quartiles_dist))

#Run the model quartiles (with interactions)

```

```

resal_disqgs0=glmer(aggression_level ~
  quartile_dist +abs_groupsize+quartile_dist*abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=quartiles_dist)

print(summary(resal_disqgs0))

#Run the model quartiles
resal_disqgs=glmer(aggression_level ~
  quartile_dist +abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=quartiles_dist)

print(summary(resal_disqgs))

cat("\n\n\n Comparison of Qs dist + group size model to null model\n\n")
print(anova(resal.nullqdis,resal_disqgs, test="Chisq"))

plotLMER.fnc(resal_disqgs,ylimit=0:1,lockYlim=TRUE,linecolor="red",
  lwd=4,xlabel="Quartiles distance",
  ylabel="Probability of highly aggressive encounter")

#####
#####
#####
#####
####          SUMMARY OF RESULTS          #####
####          #####
#####
#####

cat("\n\n\n\n\n SUMMARY OF RESULTS \n\n\n\n\n")

cat("\n\n\n\n Models with the full data set (108 IGEs in this case) \n\n\n\n")
aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al

sjp.glmer(resal_gsud, type="pred", facet.grid=FALSE, vars="abs_UD190",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resal_gs, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resal_gs2, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resal_gsud, type="pred", facet.grid=FALSE, vars="durationIGE",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resal_gsds, type="pred", facet.grid=FALSE, vars="abs_distancetocorearea",
  geom.colors = "bw",show.ci=TRUE)

```

```

sjp.glmer(resal_cyngs, type="pred", facet.grid=FALSE, vars="core_yn",
  geom.colors = "bw",show.ci=TRUE)

cat("\n\n\n Q1 dis models \n\n\n")
aictab(cand.set=modelsQ1dis, modnames = ModnamesQ1dis, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_Q1dis

sjp.glmer(resal_q1disgs, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)
sjp.glmer(resal_q1disgs, type="pred", facet.grid=FALSE, vars="abs_distancetocorearea",
  geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resal_q1disgs, type="pred", facet.grid=FALSE, vars="durationIGE",
  geom.colors = "bw",show.ci=TRUE)

table(factors_original$aggression_level,
  factors_original$dyad)

cat("\n\n\n\n What is the relationship between decided-undecided encounters and level of aggression?\n\n\n")

##I NEED TO CHANGE THIS FROM aggression_yn to aggression_level

#0=IGE without aggression; 1=contact IGE IGE
ggplot(factors_original, aes(x=decided_undecided, fill=aggression_level))+
  geom_bar(position="fill")+
  ylab("proportion")

Table<-table(factors_original$aggression_level,
  factors_original$decided_undecided)
rownames(Table)<-c("Non-contact IGE","contact IGE")
colnames(Table)<-c("Undecided","Decided")
Table

pb1r1<-(factors_original[factors_original$dyad=="pb1r1",])
Table_pb1r1<-table(pb1r1$aggression_level,
  pb1r1$decided_undecided)
rownames(Table_pb1r1)<-c("Non-contact IGE","contact IGE")
colnames(Table_pb1r1)<-c("Undecided","Decided")

r1r2<-(factors_original[factors_original$dyad=="r1r2",])
Table_r1r2<-table(r1r2$aggression_level,
  r1r2$decided_undecided)
rownames(Table_r1r2)<-c("Non-contact IGE","contact IGE")
colnames(Table_r1r2)<-c("Undecided","Decided")

pb1r2<-(factors_original[factors_original$dyad=="pb1r2",])

Table_pb1r2<-table(pb1r2$aggression_level,
  pb1r2$decided_undecided)
rownames(Table_pb1r2)<-c("Non-contact IGE","contact IGE")

```

```
colnames(Table_pb1r2)<-c("Undecided")

Table_pb1r1
Table_r1r2
Table_pb1r2

chisq.test(Table_pb1r1)
chisq.test(Table_r1r2)
#There is no reason to believe that outcome (decided vs draw) and high/low leve; of aggression are related

ggplot(factors_original, aes(x=core_yn, fill=aggression_level))+
  geom_bar(position="fill")+
  ylab("proportion")

Table1<-table(factors_original$aggression_level,
              factors_original$core_yn)
rownames(Table)<-c("Non-contact IGE","contact IGE")
colnames(Table)<-c("Both","None","One")
Table1

chisq.test(Table1)
```

2.3.5. EXPLORATION OF HOW DIFFERENCES IN GROUP SIZE AND LOCATION-BASED PAYOFFS AFFECT INTERGROUP ENCOUNTER DURATION

```
#####DURATIION OF IGE EXPLORATION###
install.packages("ggplot2")
library(ggplot2)
install.packages("car")#Package to check regression "quality"
library(car)
install.packages("ppcor")
library(ppcor)

setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()
dir()

## Upload data (when involved in parenthesis, the assigned variable/dataframe/etc is also printed in addition to be assigned)

factors_original<-read.csv("factors_originalv1.csv")

###Convert variables to the appropriate format
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dtyad<- factor(factors_original$dtyad)
```



```

nf1<-NovtoFeb1$durationIGE
aj1<-AprtoJun1$durationIGE

kruskal.test(list(nf1,aj1))

#R1-R2
cr1r2<-(change[change$dyad=="r1r2",])

r1r2$month<-factor(r1r2$month, levels=c("11", "12", "1", "2", "4", "5", "6", "7"))

boxplot(r1r2$durationIGE~ r1r2$month,ylab ="Duration IGE (min)",
        las=2,col=c("grey", "grey", "grey", "grey", "white", "white", "white", "white"),
        names = c("Nov.15", "Dec.15", "Jan.16", "Feb.16", "Apr.16", "May.16", "Jun.16", "Jul.16"), at =c(1,2,3,4,
6,7,8,9))

boxplot(durationIGE~ control_endchange,
        data = cr1r2)

NovtoFeb2 <- subset(cr1r2, month >= 11 | month < 3)
NovtoFeb2$month
AprtoJun2 <- subset(cr1r2, month<8 & month>3)
AprtoJun2$month
summary(NovtoFeb2$durationIGE)
hist(NovtoFeb2$durationIGE)
str(NovtoFeb2$durationIGE)
summary(AprtoJun2$durationIGE)
hist(AprtoJun2$durationIGE)
str(AprtoJun2$durationIGE)

nf2<-NovtoFeb2$durationIGE
aj2<-AprtoJun2$durationIGE

kruskal.test(list(nf2,aj2))

cat("\n\n\n\n\n\n\n Partial correlations for PB1-R1\n\n\n\n\n\n\n")

##Duration & Group size
durgs_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_groupsize)
pcor(durgs_pb1r1, method="pearson")
pcor(durgs_pb1r1, method="spearman")

##Graph
plot(x = pb1r1$abs_groupsize,
     y = pb1r1$durationIGE,
     xlab = "Absolute group size (No.Individuals)",
     ylab = "Duration (min)")

M0 <- lm(durationIGE~ abs_groupsize,
        data = pb1r1)
abline(M0, lwd = 3)
summary(M0)

```

##Duration & Intensity of use

```
durud_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_UD190)
pcor(durud_pb1r1, method="pearson")
pcor(durud_pb1r1, method="spearman")
```

```
plot(x = pb1r1$abs_UD190,
     y = pb1r1$durationIGE,
     xlab = "Absolute intensity of use (%)",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_UD190,
        data = pb1r1)
abline(M0, lwd = 3)
summary(M0)
```

##Duration & distance to core

```
durds_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_distancetocorearea)
pcor(durds_pb1r1, method="pearson")
pcor(durds_pb1r1, method="spearman")
```

```
plot(x = pb1r1$abs_distancetocorearea,
     y = pb1r1$durationIGE,
     xlab = "Absolute distance to core (m)",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_distancetocorearea,
        data = pb1r1)
abline(M0, lwd = 3)
summary(M0)
```

#Core/no core

```
boxplot(durationIGE~ core_yn,
        data = pb1r1)
b_data<-pb1r1[pb1r1$core_yn=="b",]
b<-b_data$durationIGE
y_data<-pb1r1[pb1r1$core_yn=="y",]
y<-y_data$durationIGE
n_data<-pb1r1[pb1r1$core_yn=="n",]
n<-n_data$durationIGE
```

```
kruskal.test(list(b, y, n))
```

```
#High intensity of use VS low intensity of use
pb1r1_iu<-(pb1r1[pb1r1$quartile_UD!="2",])
```



```
durud_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_UD190)
pcor(durud_r1r2, method="pearson")
pcor(durud_r1r2, method="spearman")

plot(x = r1r2$abs_UD190,
     y = r1r2$durationIGE,
     xlab = "Absolute intensity of use(%)",
     ylab = "Duration(min)")

M0 <- lm(durationIGE~ abs_UD190,
        data = r1r2)
abline(M0, lwd = 3)
summary(M0)

###Duration & distance to core

durds_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_distancetocorearea)
pcor(durds_r1r2, method="pearson")
pcor(durds_r1r2, method="spearman")

plot(x = r1r2$abs_distancetocorearea,
     y = r1r2$durationIGE,
     xlab = "Absolute distance to core (m)",
     ylab = "Duration (min)")

M0 <- lm(durationIGE~ abs_distancetocorearea,
        data = r1r2)
abline(M0, lwd = 3)
summary(M0)

#Core/no core

boxplot(durationIGE~ core_yn,
        data = r1r2,
        main="R1-R2",
        xlab="Categorical distance to core",
        ylab="Duration of IGE (min.)")

b_data<-r1r2[r1r2$core_yn=="b",]
b<-b_data$durationIGE
y_data<-r1r2[r1r2$core_yn=="y",]
y<-y_data$durationIGE
n_data<-r1r2[r1r2$core_yn=="n",]
n<-n_data$durationIGE

kruskal.test(list(b, y, n))
kruskal.test(list(y, n))#Eliminating b(only 1 IGE)

#High intensity of use VS low intensity of use
r1r2_iu<-(r1r2[r1r2$quartile_UD!="2",])
```

```

r1r2_iu<-r1r2_iu[r1r2_iu$excl_quartilesUD=="1",] #From the previous result, take only the ones with low
abs_UD

r1r2_iu$quartile_UD<-factor(r1r2_iu$quartile_UD, levels=c("1", "3"))
boxplot(r1r2_iu$durationIGE~ r1r2_iu$quartile_UD, names = c("Low","High"),ylab ="Duration IGE (min)",
xlab="Intensity of use of IGE location")

lowiu_r1r2_iu<-r1r2_iu[r1r2_iu$quartile_UD=="1",]
Low<-lowiu_r1r2_iu$durationIGE
highiu_r1r2_iu<-r1r2_iu[r1r2_iu$quartile_UD=="3",]
High<-highiu_r1r2_iu$durationIGE

kruskal.test(list(Low,High))

#Close VS Far from core areas

r1r2_dis<-(r1r2[r1r2$quartile_dist!="2",])

r1r2_dis$quartile_dist<-factor(r1r2_dis$quartile_dist, levels=c("1", "3"))
boxplot(r1r2_dis$durationIGE~ r1r2_dis$quartile_dist, names = c("Short","Long"),ylab ="Duration IGE (min)",
xlab="Distance to closest core area")

low_r1r2_dis<-r1r2_dis[r1r2_dis$quartile_UD=="1",]
Sh<-low_r1r2_dis$durationIGE
high_r1r2_dis<-r1r2_dis[r1r2_dis$quartile_UD=="3",]
Lo<-high_r1r2_dis$durationIGE

kruskal.test(list(Sh,Lo))

##PB1-R2
pb1r2$durationIGE
pb1r2$abs_groupsize
pb1r2$abs_UD190
pb1r2$abs_distancetocorearea
pb1r2$core_yn

#####Duration per dyad#####
boxplot(durationIGE~ dyad,
      data = factors_original)

dpb1r1<-pb1r1$durationIGE
dr1r2<-r1r2$durationIGE
dpb1r2<-pb1r2$durationIGE

kruskal.test(list(dpb1r1, dr1r2, dpb1r2))

```

```
geom_boxplot()
```

```
ggplot(factors_original, aes(x=aggression_yn,y=durationIGE))+  
  geom_boxplot()+  
  facet_wrap(~dyad)
```

```
cat("\n Residuals VS Fitted values (https://onlinecourses.science.psu.edu/stat501/node/36 [Accessed 11th Sep 2017] n\")
```

```
# Here are the characteristics of a well-behaved residual vs. fits plot and what they suggest about the appropriateness of the simple linear regression model:
```

```
# The residuals "bounce randomly" around the 0 line. This suggests that the assumption that the relationship is linear is reasonable.
```

```
# The residuals roughly form a "horizontal band" around the 0 line. This suggests that the variances of the error terms are equal.
```

```
# No one residual "stands out" from the basic random pattern of residuals. This suggests that there are no outliers.
```

```
cat("\n\n\n\n What if we remove the 2 IGEs PB1-R2?\n\n\n\n")
```

```
##Partial correlation
```

```
durgs<-data.frame(nopb1r2$durationIGE,nopb1r2$abs_groupsize)  
pcor(durgs, method="pearson")  
cor(nopb1r2$durationIGE,nopb1r2$abs_groupsize)
```

```
##Graph
```

```
plot(x = nopb1r2$abs_groupsize,  
     y = nopb1r2$durationIGE,  
     xlab = "Absolute group size",  
     ylab = "Duration")
```

```
M0 <- lm(durationIGE~abs_groupsize, data = nopb1r2)  
abline(M0, lwd = 3)
```

```
summary(M0)  
plot(M0)
```

```
cat("\n\n\n\n\n\n\n\n Duration and use of space difference\n\n\n\n\n\n\n\n")
```

```
##Partial correlation
```

```
durud<-data.frame(factors_original$durationIGE,factors_original$abs_UD190)  
pcor(durud, method="pearson")
```

```
##Graph
```

```

plot(x = factors_original$abs_UD190,
     y = factors_original$durationIGE,
     xlab = "Absolute use of space",
     ylab = "Duration")

M0 <- lm(durationIGE~ abs_UD190,
factors_original)
abline(M0, lwd = 3)

summary(M0)

plot(M0)

cat("\n\n\n\n\n\n\n\n Duration and distance to core \n\n\n\n\n\n\n\n")

##Partial correlation

durds<-data.frame(factors_original$durationIGE,factors_original$abs_distancetocorearea)
pcor(durds, method="pearson")

##Graph
plot(x = factors_original$abs_distancetocorearea,
     y = factors_original$durationIGE,
     xlab = "Absolute distance to core",
     ylab = "Duration")

M0 <- lm(durationIGE~abs_distancetocorearea, factors_original)
abline(M0, lwd = 3)

summary(M0)

plot(M0)

cat("\n\n\n\n\n\n\n\n Duration and dyad \n\n\n\n\n\n\n\n")

ggplot(factors_original, aes(x=durationIGE))+
  geom_histogram()+
  facet_wrap(~dyad)

boxplot(durationIGE~ dyad,
        data = factors_original)

summary(factors_original$durationIGE[factors_original$dyad=="pb1r1"])
summary(factors_original$durationIGE[factors_original$dyad=="r1r2"])
summary(factors_original$durationIGE[factors_original$dyad=="pb1r2"])

cat("\n\n\n\n\n\n\n\n Duration and decided vs undecided encounters \n\n\n\n\n\n\n\n")

ggplot(factors_original, aes(x=durationIGE))+

```

```
geom_histogram()+  
facet_wrap(~decided_undecided)  
  
boxplot(durationIGE~ decided_undecided,  
        data = factors_original)  
  
summary(factors_original$durationIGE[factors_original$decided_undecided=="1"])  
summary(factors_original$durationIGE[factors_original$decided_undecided=="0"])
```

2.4. Testing alternative methods to select focal groups in models investigating probability of winning an encounter: R script

```
## download packages  
# installing/loading the package:  
if(!require(installr)) {  
  install.packages("installr"); require(installr)} #load / install+load installr  
  
# using the package:  
updateR() # this will start the updating process of your R installation. It will check for newer versions, and if one  
is available, will guide you through the decisions you'd need to make.  
  
install.packages("lme4")#Package that allows to calculate the glms  
install.packages("car")#Package to check regression "quality"  
install.packages("ppcor")#To check for correlations between independent variables  
install.packages("ggplot2")# To plot independent variables and glms  
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account  
for the variation)  
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc  
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)  
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function  
  
library(lme4)  
library(car)  
library(ppcor)  
library(ggplot2)  
library(modEvA)  
library(languageR)  
library(AICcmodavg)  
library(MuMIn)  
  
#Set directory  
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")  
getwd()
```

```
> cat("\n\n\n\n\n\n\n\n\n\n\n\n\n METHOD: Random flipping keeping 2 dyads \n\n\n\n\n\n\n\n\n\n\n\n\n")
```

2.4.1. METHOD: RANDOM FLIPPING KEEPING 2 DYADS

```
>
> # This seems to be the method employed in Crofoot et al 2008; Markham et al 2012 and K
och et al 2016 (But see next method)
> # The problem of this methods as far as I understand is that it artificially inflates
the variability, by keeping a random
> # factor with 2 categories (dyad) when the flipping mathematically doubles the random
factor
>
> ## Upload data
> factors_original<-read.csv("factors_original.csv")
>
> ##### RANDOM FLIPPING #####
>
> #Checking the original data
> factors_original$winner_analysis
[1] 0 1 0 0 1 1 0 NA 1 NA 1 1 0 0 0 0 NA NA NA 1 1 1 0 1 0 0 0
0 0 1 0 0 0 1 0 0 NA 0 1 0 0 1 0 1 0 1
[47] 0 0 0 1 0 0 0 1 0 1 0 1 0 NA 0 NA NA 1 0 0 0 0 0 1 1 0 1
0 1 0 0 NA NA 1 1 0 1 1 0 0 NA 0 0 0 1 1
[93] 1 0 0 1 0 0 NA 1 NA 0 0 NA 1 1 0 NA 0 NA 0 NA 0 0 0 NA 0 NA NA N
A 1 0 0 NA 1 0 1 NA 0 1 0 0 NA NA 0 0 1 0
[139] 0 NA NA NA 0 0 NA 1 NA 1 0 1 NA 0 0 0 1 0 NA NA 0 1 0 1 NA
> factors_original$rel_groupsize
[1] -15 -15 NA -15 14 -16 NA NA 14 -16 NA 14 -16 -16 -16 15 15 NA NA NA -1
6 15 15 NA NA 14 15 NA NA -15 -16 -16 -16 -16
[35] -16 NA NA -16 -16 -16 -15 14 NA 15 15 NA -16 -16 NA -16 -16 -16 -16 1
2 12 12 12 NA -16 12 12 NA NA -16 NA NA NA
[69] NA NA -16 -16 -16 -16 -16 12 12 -16 -16 -16 -16 12 -16 -15 11 12 12 12 1
2 -17 -16 12 -15 -15 -15 -15 -15 -15 NA -4 11
[103] 11 NA -14 11 -14 -14 -14 -15 -15 -14 11 11 12 -15 -15 -15 11 -15 -15 -15 -1
5 -14 -14 14 -16 -15 14 -14 12 -13 -14 12 -14 -13
[137] -13 -13 -10 -10 -10 -3 -14 -13 -14 12 -11 10 11 11 NA -13 -13 NA 10 NA N
A NA NA NA -14 NA 12
>
>
>
>
```

```

> # Flip the variables randomly
>
> set.seed(123456)
>
> randomflips = runif(nrow(factors_original),0,1)>.5
> factors_original$winner_analysis[ randomflips] <- 1-factors_original$winner_analysis
[ randomflips]
> factors_original$rel_groupsize[ randomflips] <- -factors_original$rel_groupsize[
randomflips]
> factors_original$rel_UD190[randomflips] <- -factors_original$rel_UD190[ randomflip
s]
> factors_original$rel_distancetocorearea[randomflips] <- -factors_original$ rel_dist
ancetocorearea[ randomflips]
>
>
> #Checking that the flipping worked
> factors_original$winner_analysis
[1] 1 0 0 0 1 1 1 NA 0 NA 0 0 1 1 1 1 NA NA NA 0 1 1 0 1 0 1 1
1 1 1 1 1 0 1 1 0 NA 1 0 1 0 0 1 1 1 1
[47] 1 1 1 1 0 1 1 0 1 0 1 0 0 NA 0 NA NA 1 0 1 0 0 0 1 1 1 0
0 0 0 1 NA NA 0 1 0 0 0 1 0 NA 1 1 0 1 1
[93] 1 0 0 1 1 1 NA 1 NA 1 0 NA 0 0 1 NA 1 NA 0 NA 0 0 0 NA 0 NA NA N
A 1 0 1 NA 0 0 1 NA 1 1 0 1 NA NA 1 0 1 1
[139] 0 NA NA NA 1 1 NA 1 NA 0 0 0 NA 1 0 1 0 0 NA NA 0 1 1 1 NA
> factors_original$rel_groupsize
[1] 15 15 NA -15 14 -16 NA NA -14 -16 NA -14 16 16 16 -15 -15 NA NA NA -1
6 15 15 NA NA -14 -15 NA NA -15 16 16 -16 -16
[35] 16 NA NA 16 16 16 -15 -14 NA 15 -15 NA 16 16 NA -16 -16 16 16 16 -1
2 -12 -12 -12 NA -16 12 12 NA NA -16 NA NA NA
[69] NA NA -16 16 16 -16 16 12 -12 -16 -16 16 -16 12 16 15 -11 12 12 -12 -1
2 -17 -16 12 -15 -15 -15 -15 15 15 -15 NA -4 -11
[103] 11 NA 14 -11 14 -14 14 15 -15 -14 11 11 12 -15 -15 -15 11 15 -15 -15 1
5 14 14 14 -16 -15 -14 -14 12 13 -14 -12 14 -13
[137] -13 13 -10 -10 10 3 14 13 -14 12 11 -10 11 -11 NA 13 -13 NA -10 NA N
A NA NA NA 14 NA 12
>
>
>
> ###Convert variables to the appropriate format
> factors_original$num_obs<- as.numeric(factors_original$num_obs)
> factors_original$dyad<- factor(factors_original$dyad)
> factors_original$winner_analysis<- factor(factors_original$winner_analysis)
> factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
> factors_original$rel_groupsize<- as.numeric(factors_original$rel_groupsize)
> factors_original$rel_UD190<- as.numeric(factors_original$rel_UD190)
> factors_original$rel_distancetocorearea<- as.numeric(factors_original$rel_distancetoc
orearea)

> #Eliminating NAs (otherwise when calculating the null models the sample size is differ
ent and the comparison cannot be made)
> missingrows = is.na(factors_original$rel_groupsize)
> factors_original = factors_original[!missingrows,]
> missingrows = is.na(factors_original$winner_analysis)
> factors_original= factors_original[!missingrows,]
>
>
>
> cat("\n\n\n\n\n\n Checking possible control variables: Encounter duration and number o
f observers \n\n\n\n\n\n")

```

Checking possible control variables: Encounter duration and number of observers

```

>
>
> #Model with duration as a fixed factor
> res_cv=glmer(winner_analysis ~
+               durationIGE+num_obs+
+               (1|dyad), family="binomial", data=factors_original)
>
> print(summary(res_cv))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmer
Mod']
Family: binomial ( logit )
Formula: winner_analysis ~ durationIGE + num_obs + (1 | dyad)
Data: factors_original

      AIC      BIC   logLik deviance df.resid
  149.0    159.6   -70.5    141.0        99

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.3336 -1.0895  0.7960  0.9047  1.0587

Random effects:
Groups Name      Variance Std.Dev.
dyad  (Intercept) 2.5e-15  5e-08
Number of obs: 103, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.035984   0.528624  -0.068   0.946
durationIGE -0.002170   0.006462  -0.336   0.737
num_obs      0.164858   0.221337   0.745   0.456

Correlation of Fixed Effects:
              (Intr) drtIGE
durationIGE -0.327
num_obs     -0.700 -0.346
>
> #Comparison between the null model and the model with duration as a fixed factor
> res.null=glmer(winner_analysis ~ 1 +(1|dyad), family="binomial", data=factors_origina
1)
> print(anova(res.null,res_cv, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_cv: winner_analysis ~ durationIGE + num_obs + (1 | dyad)
      Df    AIC    BIC   logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 145.53 150.80 -70.767   141.53
res_cv    4 149.04 159.58 -70.522   141.04 0.4887     2    0.7832
>

```

```

> #Starting a list to calculate AICs to compare between all the models
> models<-list()
> models[[1]]<-res.null
> Modnames <- "Null model"
>
>
> #Calculating R2
> r2_null<-r.squaredGLMM(res.null)
The result is correct only if all data used by the model has not changed since model was
fitted.
>
> R2<-r2_null
>
>
>
> #There is no significant relationships between the potential control variables "durati
onIGE" and whether the focal
> #group wins an encounter. Thus, they will not be used as a control variable in these a
nalyzes

> cat("\n\n\n\n\n Group size and Use of space models \n\n\n\n\n")

```

Group size and Use of space models

```

>
>
>
> cat("\n\n\n Does group size combined with use of space affects the chances of winning
an encounter?\n\n\n")

```

Does group size combined with use of space affects the chances of winning an encounter?

```

>
> # Response: winner_analysis (binary,1=Focal group wins, 0= Focal group loses)
> # Fixed effects: rel_groupsize (Number of adult individuals at the Focal Group- Number
of adult individuals at the
> # opponent group) and rel_UD190 (Usage of space of G1 on the starting point of the enc
ounter-
> # Usage of space G2 on the starting point of the encounter. Usage of space was calcula
te with BBMM in R,
> # with cell.size 190. The BBMM where calculated by calendar month and the values were
taken from the calendar
> # month previous to the IGE (e.g. if the encounter was in May, the use of space is the
one of April)
> #Random effect: 'dyad', 2 levels.
> #Hypothesis: The probability of winning an encounter varies with the relative size of
the group

```

```

> #with the group with bigger size more likely to win the encounter (i.e.in this particu
lar data set,
> #greater positive rel_groupsize) and the group that uses the area more, more likely to
win.
>
> #Checking colinearity (close to 1 is good, over 4 is a problem)
> vif(glm(winner_analysis ~ rel_groupsize+ rel_UD190, family="binomial", data=factors_o
riginal))
rel_groupsize      rel_UD190
      1.008479      1.008479
>
>
> #Group size & Relative UD Model
> res_gsud=glmer(winner_analysis ~
+               rel_groupsize+
+               rel_UD190+rel_groupsize*rel_UD190+
+               (1|dyad), family="binomial", data=factors_original)
Warning messages:
1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model failed to converge with max|grad| = 0.00185828 (tol = 0.001, component 1)
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
  - Rescale variables?
>
> print(summary(res_gsud))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmer
Mod']

Family: binomial ( logit )
Formula: winner_analysis ~ rel_groupsize + rel_UD190 + rel_groupsize *      rel_UD190 +
(1 | dyad)
Data: factors_original

      AIC      BIC  logLik deviance df.resid
    148.0    161.1   -69.0    138.0      98

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.7399 -1.0108  0.6379  0.9277  1.3106

Random effects:
Groups Name      Variance Std.Dev.
dyad  (Intercept) 0.04067  0.2017
Number of obs: 103, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.1650207  0.2584675   0.638   0.523
rel_groupsize    0.0108344  0.0144994   0.747   0.455
rel_UD190        0.0080896  0.0055165   1.466   0.143
rel_groupsize:rel_UD190 0.0002330  0.0004065   0.573   0.567

Correlation of Fixed Effects:
              (Intr) r1_grp r_UD19
rel_groupsz   0.025
rel_UD190    -0.059  0.111
r1_g:_UD190   0.022 -0.127 -0.134
convergence code: 0
Model failed to converge with max|grad| = 0.00185828 (tol = 0.001, component 1)
Model is nearly unidentifiable: very large eigenvalue
  - Rescale variables?

```



```

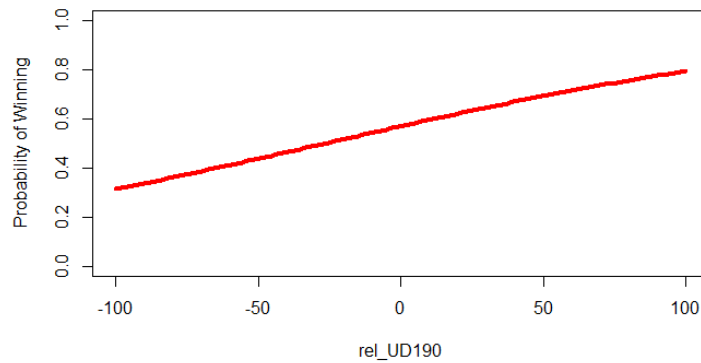
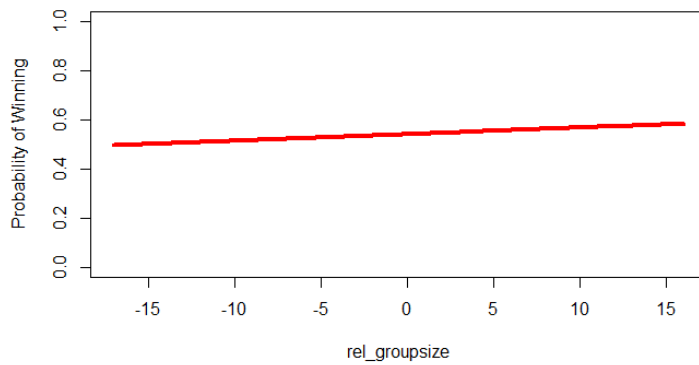
>
>
> cat("\n\n Comparison of Group size & Relative UD model to null model\n\n")

Comparison of Group size & Relative UD model to null model

> print(anova(res.null,res_gsud, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_gsud: winner_analysis ~ rel_groupsize + rel_UD190 + rel_groupsize *
res_gsud:      rel_UD190 + (1 | dyad)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
res.null  2 145.53 150.80 -70.767   141.53
res_gsud  5 147.97 161.15 -68.986   137.97 3.5604      3      0.313
>
>
> #Calculate AICs to compare between all the models
> models[[2]]<-res_gsud
> Modnames <- rbind(Modnames, "Group size and use of space model")
>
>
>
> #Calculating R2
> r2_gsud<-r.squaredGLMM(res_gsud)
The result is correct only if all data used by the model has not changed since model was
fitted.
Warning messages:
1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model failed to converge with max|grad| = 0.00102634 (tol = 0.001, component 1)
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
>
> R2<-rbind(R2,r2_gsud)
>
>
>
> #Probability plot
> plotLMER.fnc(res_gsud,ylimit=0:1,lockYlim=TRUE,linecolor="red",
+             lwd=4,xlabel="Relative group size",
+             ylabel="Probability of winning")
log odds are back-transformed to probabilities
effect size (range) for rel_groupsize is 0.08878235

```

effect size (range) for rel_UD190 is 0.4797948



```
> cat("\n\n\n\n\n Group size and distance to core area models \n\n\n\n\n")
```

Group size and distance to core area models

```
>
>
>
> cat("\n\n\n Does group size combined with distance to core area the chances of winning
an encounter?\n\n\n")
```

Does group size combined with distance to core area the chances of winning an encounter?

```

>
> # Response: winner_analysis (binary, 1=Focal group wins, 0= Focal group loses)
> # Fixed effects: rel_groupsize (Number of adult individuals at the Focal Group- Number
of adult individuals at the
> #opponent group) and rel_distancetocorearea (Usage of space of G1 on the starting poin
t of the encounter-
> # Usage of space G2 on the starting point of the encounter. Usage of space was calcula
te with BBMM in R,
> # with cell.size 190. The BBMM where calculated by calendar month and the values were
taken from the calendar
> # month previous to the IGE (e.g. if the encounter was in May, the use of space is the
one of April)
> #Random effect: 'dyad', 2 levels.
> #Hypothesis: The probability of winning an encounter varies with the relative size of
the group
> #with the group with bigger size more likely to win the encounter (i.e.in this particu
lar data set,
> #greater positive rel_groupsize) and the group that is closer to its core area, more l
ikely to win.
>
> #Checking colinearity (close to 1 is good, over 4 is a problem)
> vif(glm(winner_analysis ~ rel_groupsize+ rel_distancetocorearea, family="binomial", d
ata=factors_original))
               rel_groupsize rel_distancetocorearea
               1.199582      1.199582
>
>
> #Group size & Relative distance to core area Model
> res_gsdis=glmer(winner_analysis ~
+               rel_groupsize+
+               rel_distancetocorearea+
+               (1|dyad), family="binomial", data=factors_original)
Warning messages:
1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model failed to converge with max|grad| = 0.00120554 (tol = 0.001, component 1)
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
  - Rescale variables?
>
> print(summary(res_gsdis))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmer
Mod']

Family: binomial ( logit )
Formula: winner_analysis ~ rel_groupsize + rel_distancetocorearea + (1 | dyad)
Data: factors_original

            AIC      BIC   logLik deviance df.resid
        148.4    158.9    -70.2    140.4      99

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.3301 -1.0755  0.7507  0.9106  1.1275

Random effects:
Groups Name      Variance Std.Dev.
dyad (Intercept) 0.0267   0.1634
Number of obs: 103, groups: dyad, 2

```

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.1880731	0.2417677	0.778	0.437
rel_groupsize	0.0150781	0.0153801	0.980	0.327
rel_distancetocorearea	-0.0005266	0.0007082	-0.744	0.457

Correlation of Fixed Effects:

```
(Intr) r1_grp
rel_groupsz 0.000
r1_dstnctcr 0.042 -0.394
convergence code: 0
```

Model failed to converge with max|grad| = 0.00120554 (tol = 0.001, component 1)

Model is nearly unidentifiable: very large eigenvalue

- Rescale variables?

>

>

```
> cat("\n\n Comparison of Group size & Relative distance to core area model to null mo
del\n\n")
```

Comparison of Group size & Relative distance to core area model to null model

```
> print(anova(res.null,res_gsdis, test="Chisq"))
```

Data: factors_original

Models:

res.null: winner_analysis ~ 1 + (1 | dyad)

res_gsdis: winner_analysis ~ rel_groupsize + rel_distancetocorearea + (1 |

res_gsdis: dyad)

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
res.null	2	145.53	150.80	-70.767	141.53				
res_gsdis	4	148.41	158.94	-70.203	140.41	1.1266		2	0.5693

>

```
> #Including results in AIC list
```

```
> models[[3]]<-res_gsdis
```

```
> Modnames <- rbind(Modnames, "Group size and distance to core area model")
```

>

>

```
> #Calculating R2
```

```
> r2_gsdis<-r.squaredGLMM(res_gsdis)
```

The result is correct only if all data used by the model has not changed since model was fitted.

Warning message:

```
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
```

```
Model is nearly unidentifiable: very large eigenvalue
```

```
- Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
```

```
- Rescale variables?
```

>

```
> R2<-rbind(R2,r2_gsdis)
```

>

>

```
> #Probability plot
```

```
> plotLMER.fnc(res_gsdis,ylimit=0:1,lockYlim=TRUE,linecolor="red",
```

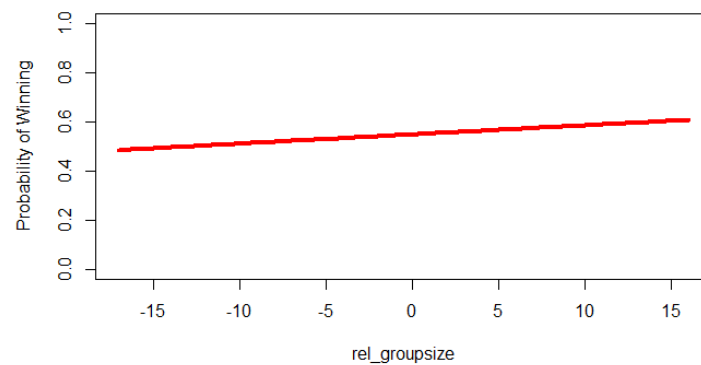
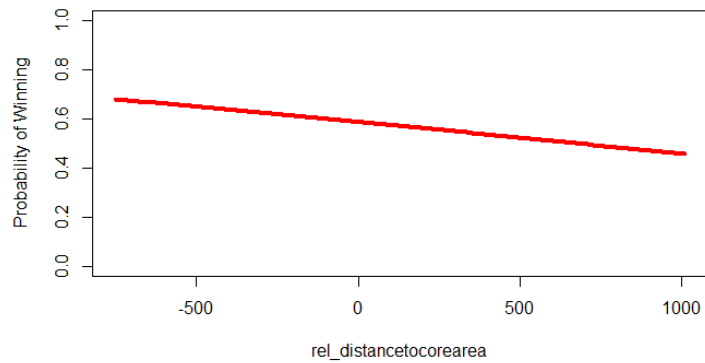
```
+ lwd=4,xlabel="Relative group size",
```

```
+ ylabel="Probability of Winning")
```

log odds are back-transformed to probabilities

effect size (range) for rel_groupsize is 0.1227094

effect size (range) for rel_distancetocorearea is 0.2234722



```
> #####
#####
>
> cat("\n\n\n\n\n RESULTS\n\n\n\n\n")
```

RESULTS

```
>
> #####
#####
> ## Best model according to AIC
>
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcwt	Cum.Wt	LL
Null model	2	145.65	0.00	0.70	0.70	-70.77
Group size and use of space model	5	148.59	2.94	0.16	0.86	-68.99
Group size and distance to core area model	4	148.81	3.16	0.14	1.00	-70.20

Warning message:

```
In data.row.names(row.names, rowsi, i) :
  some row.names duplicated: 3 --> row.names NOT used
>
> ## Best model according to R2
> R2
      R2m      R2c
R2      0.00000000 0.008077611
r2_gsud 0.04591970 0.057570373
r2_gsdis 0.01354437 0.021484504
>
>
>
>
> cat("\n\n what variability does dyad explain? \n\n")
```

What variability does dyad explain?

```
>
>
> res_dy=glm(winner_analysis ~ dyad, family="binomial", data=factors_original)
> res.null_dy=glm(winner_analysis ~ 1, family="binomial", data=factors_original)
>
> print(summary(res_dy))
```

Call:

```
glm(formula = winner_analysis ~ dyad, family = "binomial", data = factors_original)
```

Deviance Residuals:

	Min	1Q	Median	3Q	Max
	-1.3824	-1.0891	0.9854	0.9854	1.2684

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	0.4700	0.2550	1.844	0.0653 .
dyadr1r2	-0.6813	0.4141	-1.645	0.0999 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 141.61 on 102 degrees of freedom
 Residual deviance: 138.87 on 101 degrees of freedom
 AIC: 142.87

Number of Fisher Scoring iterations: 4

```
>
> cat("\n\n Comparison between dyad model and null model\n\n")
```

```

Comparison between dyad model and null model

>
> print(anova(res.null_dy, res_dy, test="Chisq"))
Analysis of Deviance Table

Model 1: winner_analysis ~ 1
Model 2: winner_analysis ~ dyad
      Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1          102      141.61
2          101      138.87  1    2.7378    0.098 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> summary(res_dy)

Call:
glm(formula = winner_analysis ~ dyad, family = "binomial", data = factors_original)

Deviance Residuals:
      Min       1Q   Median       3Q      Max
-1.3824  -1.0891   0.9854   0.9854   1.2684

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.4700     0.2550   1.844   0.0653 .
dyadr1r2     -0.6813     0.4141  -1.645   0.0999 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

      Null deviance: 141.61  on 102  degrees of freedom
Residual deviance: 138.87  on 101  degrees of freedom
AIC: 142.87

Number of Fisher Scoring iterations: 4

>
>
> #Calculate (pseudo) R-squared statistics
>
> RsqGLM(res_dy)
$CoxSnell
[1] 0.02623014

$Nagelkerke
[1] 0.03510801

$McFadden
[1] 0.01933298

$Tjur
[1] 0.02659295

$sqPearson
[1] 0.02659295

```

```
> cat("\n\n\n\n\n\n\n\n\n\n\n METHOD: Random flipping with 4 dyads \n\n\n\n\n\n\n\n\n\n\n")
```

2.4.2. METHOD: RANDOM FLIPPING WITH 4 DYADS

```
>
> #In this case, after flipping the factors randomly, those that had been swiftly were a
signed the other dyadic direction (so pb1r1 became r1pb1 when the
> # factors had been flipped from pb1-r1 to r1-pb1). It still inflates the number of dya
ds artificially to 4 instead of the 2 original dyads, but corrects
> # for the artificially augmented variability from the first method
>
> ## Upload data
> factors_original<-read.csv("factors_original_flippedDoubledDyads.csv") #A new dataset
was created manually coping the one flipped in R, switching dyads when corresponding
>
>
>
> cat("\n\n\n\n\n Checking possible control variables: Encounter duration and number o
f observers \n\n\n\n\n")
```

Checking possible control variables: Encounter duration and number of observers

```
>
>
> #Model with duration as a fixed factor
> res_cv=glmer(winner_analysis ~
+               durationIGE+num_obs+
+               (1|dyad2), family="binomial", data=factors_original)
>
```



```

> print(summary(res_cv))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmer
Mod']
Family: binomial ( logit )
Formula: winner_analysis ~ durationIGE + num_obs + (1 | dyad2)
Data: factors_original

      AIC      BIC   logLik deviance df.resid
  147.3   157.8   -69.6   139.3     99

Scaled residuals:
    Min      1Q   Median      3Q      Max
-1.5304 -1.0287  0.6916  0.9055  1.3068

Random effects:
Groups Name      Variance Std.Dev.
dyad2 (Intercept) 0.2185   0.4675
Number of obs: 103, groups: dyad2, 4

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.047398   0.597626   0.079   0.937
durationIGE -0.002727   0.006730  -0.405   0.685
num_obs      0.109909   0.240739   0.456   0.648

Correlation of Fixed Effects:
          (Intr) drtIGE
durationIGE -0.282
num_obs     -0.649 -0.356
>
> #Comparison between the null model and the model with duration as a fixed factor
> res.null=glmer(winner_analysis ~ 1 +(1|dyad2), family="binomial", data=factors_origin
al)
> print(anova(res.null,res_cv, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad2)
res_cv: winner_analysis ~ durationIGE + num_obs + (1 | dyad2)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
res.null  2 143.56 148.83 -69.778   139.56
res_cv    4 147.28 157.82 -69.640   139.28 0.2754     2    0.8714
>
> #Starting a list to calculate AICs to compare between all the models
> models<-list()
> models[[1]]<-res.null
> Modnames <- "Null model"
>
>
> #Calculating R2
> r2_null<-r.squaredGLMM(res.null)
Error in glmer(formula = winner_analysis ~ (1 | dyad2) + (1 | gl(104, :
fitting model with the observation-level random effect term failed. Add the term manua
lly
In addition: Warning message:
In value[[3L]](cond) : (p <- ncol(X)) == ncol(Y) is not TRUE
>
> R2<-r2_null
>
>
>

```

```

> #There is no significant relationships between the potential control variables "durati
onIGE" and whether the focal
> #group wins an encounter. Thus, they will not be used as a control variable in these a
nalyzes
>
>
>
>
>
> cat("\n\n\n\n\n Group size and Use of space models \n\n\n\n\n")

```

Group size and Use of space models

```

>
>
>
> cat("\n\n\n Does group size combined with use of space affects the chances of winning
an encounter?\n\n\n")

```

Does group size combined with use of space affects the chances of winning an encounter?

```

>
> # Response: winner_analysis (binary,1=Focal group wins, 0= Focal group loses)
> # Fixed effects: rel_groupsize (Number of adult individuals at the Focal Group- Number
of adult individuals at the
> # opponent group) and rel_UD190 (Usage of space of G1 on the starting point of the enc
ounter-
> # Usage of space G2 on the starting point of the encounter. Usage of space was calcula
te with BBMM in R,
> # with cell.size 190. The BBMM where calculated by calendar month and the values were
taken from the calendar
> # month previous to the IGE (e.g. if the encounter was in May, the use of space is the
one of April)
> #Random effect: 'dyad2', 2 levels.
> #Hypothesis: The probability of winning an encounter varies with the relative size of
the group
> #with the group with bigger size more likely to win the encounter (i.e.in this particu
lar data set,
> #greater positive rel_groupsize) and the group that uses the area more, more likely to
win.
>
> #Checking colinearity (close to 1 is good, over 4 is a problem)
> vif(glm(winner_analysis ~ rel_groupsize+ rel_UD190, family="binomial", data=factors_o
riginal))
rel_groupsize    rel_UD190
      1.008479      1.008479
>
>

```

```

> #Group size & Relative UD Model
> res_gsud=glmer(winner_analysis ~
+               rel_groupsize+
+               rel_UD190+
+               (1|dyad2), family="binomial", data=factors_original)
>
> print(summary(res_gsud))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmer
Mod']

Family: binomial ( logit )
Formula: winner_analysis ~ rel_groupsize + rel_UD190 + (1 | dyad2)
Data: factors_original

      AIC      BIC   logLik deviance df.resid
143.8    154.3    -67.9   135.8      99

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.4637 -1.0473  0.5567  0.8305  1.5285

Random effects:
Groups Name      Variance Std.Dev.
dyad2 (Intercept) 0.3523   0.5935
Number of obs: 103, groups: dyad2, 4

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.077892   0.369728   0.211   0.8331
rel_groupsize 0.002363   0.026460   0.089   0.9288
rel_UD190     0.010853   0.005832   1.861   0.0627 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) rl_grp
rel_groupsz  0.040
rel_UD190    -0.093 -0.020
>
>
> cat("\n\n Comparison of Group size & Relative UD model to null model\n\n")

Comparison of Group size & Relative UD model to null model

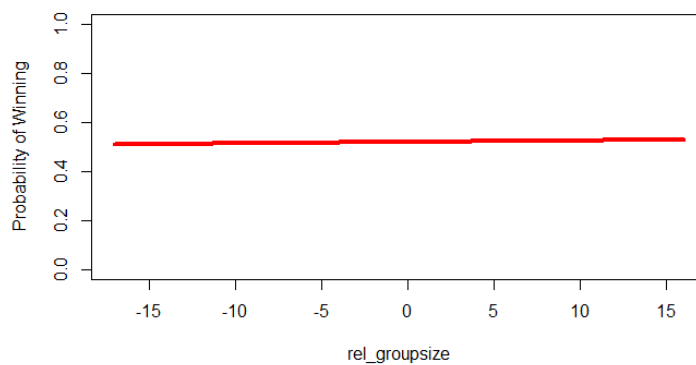
> print(anova(res.null,res_gsud, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad2)
res_gsud: winner_analysis ~ rel_groupsize + rel_UD190 + (1 | dyad2)
      Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 143.56 148.83 -69.778   139.56
res_gsud  4 143.78 154.32 -67.889   135.78 3.7777     2    0.1512
>
>
> #Calculate AICs to compare between all the models
> models[[2]]<-res_gsud
> Modnames <- rbind(Modnames, "Group size and use of space model")
>
>

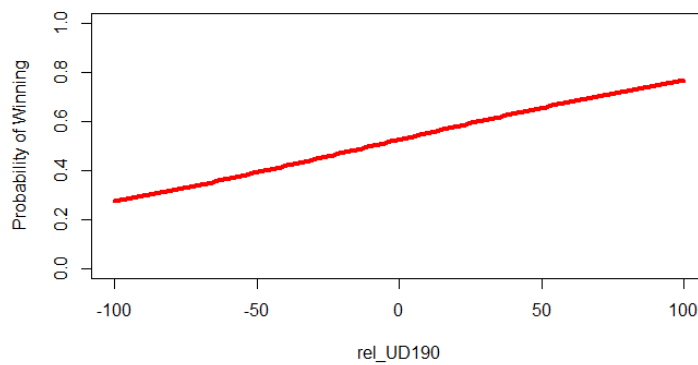
```

```

>
> #Calculating R2
> r2_gsud<-r.squaredGLMM(res_gsud)
Error in glmer(formula = winner_analysis ~ rel_groupsize + rel_UD190 + :
  fitting model with the observation-level random effect term failed. Add the term manua
11y
In addition: Warning message:
In value[[3L]](cond) : (p <- ncol(X)) == ncol(Y) is not TRUE
>
> R2<-rbind(R2,r2_gsud)
>
>
>
> #Probability plot
> plotLMER.fnc(res_gsud,ylim=0:1,lockYlim=TRUE,linecolor="red",
+             lwd=4,xlabel="Relative group size",
+             ylabel="Probability of Winning")
log odds are back-transformed to probabilities
effect size (range) for rel_groupsize is 0.0194611
effect size (range) for rel_UD190 is 0.4938252

```





```
> cat("\n\n\n\n\n Group size and distance to core area models \n\n\n\n\n")
```

Group size and distance to core area models

```
>
>
>
> cat("\n\n\n Does group size combined with distance to core area the chances of winning
an encounter?\n\n\n")
```

Does group size combined with distance to core area the chances of winning an encounter?

```
>
> # Response: winner_analysis (binary, 1=Focal group wins, 0= Focal group loses)
> # Fixed effects: rel_groupsize (Number of adult individuals at the Focal Group- Number
of adult individuals at the
> #opponent group) and rel_distancetocorearea (Usage of space of G1 on the starting point
of the encounter-
> # Usage of space G2 on the starting point of the encounter. Usage of space was calculated
with BBMM in R,
> # with cell.size 190. The BBMM were calculated by calendar month and the values were
taken from the calendar
> # month previous to the IGE (e.g. if the encounter was in May, the use of space is the
one of April)
> #Random effect: 'dyad2', 2 levels.
> #Hypothesis: The probability of winning an encounter varies with the relative size of
the group
```

```

> #with the group with bigger size more likely to win the encounter (i.e.in this particu
lar data set,
> #greater positive rel_groupsize) and the group that is closer to its core area, more l
ikely to win.
>
> #checking colinearity (close to 1 is good, over 4 is a problem)
> vif(glm(winner_analysis ~ rel_groupsize+ rel_distancetocorearea, family="binomial", d
ata=factors_original))
               rel_groupsize rel_distancetocorearea
               1.199582           1.199582
>
>
> #Group size & Relative distance to core area Model
> res_gsdis=glmer(winner_analysis ~
+               rel_groupsize+
+               rel_distancetocorearea+
+               (1|dyad2), family="binomial", data=factors_original)
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
  - Rescale variables?
>
> print(summary(res_gsdis))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmer
Mod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_groupsize + rel_distancetocorearea + (1 |      dyad2)
Data: factors_original

      AIC      BIC   logLik deviance df.resid
  145.7   156.3   -68.9   137.7      99

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.7211 -0.9699  0.5830  0.8699  1.4550

Random effects:
Groups Name      Variance Std.Dev.
dyad2 (Intercept) 0.3852   0.6207
Number of obs: 103, groups: dyad2, 4

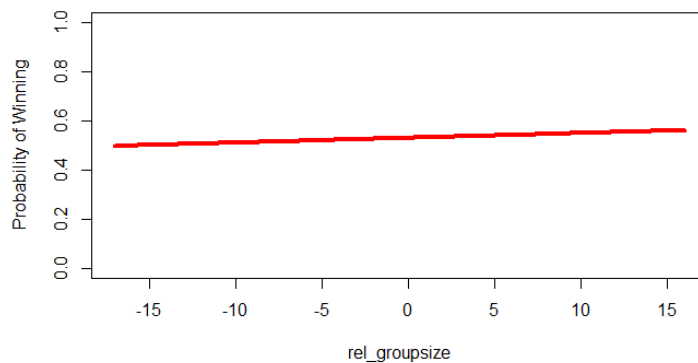
Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.1109582  0.3780423   0.294   0.769
rel_groupsize    0.0078550  0.0276419   0.284   0.776
rel_distancetocorearea -0.0010473  0.0007917  -1.323   0.186

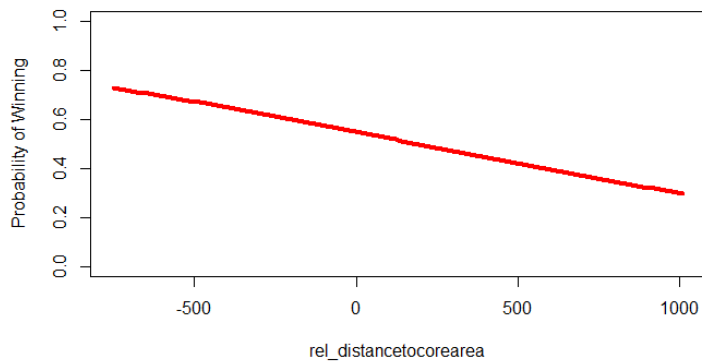
Correlation of Fixed Effects:
              (Intr) rl_grp
rel_groupsz   0.031
rl_dstnctcr   0.049 -0.116
convergence code: 0
Model is nearly unidentifiable: very large eigenvalue
  - Rescale variables?
>
>
> cat("\n\n Comparison of Group size & Relative distance to core area model to null mo
del\n\n")

```

Comparison of Group size & Relative distance to core area model to null model

```
> print(anova(res.null,res_gsdis, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad2)
res_gsdis: winner_analysis ~ rel_groupsize + rel_distancetocorearea + (1 |
res_gsdis: dyad2)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
res.null  2 143.56 148.83 -69.778   139.56      2    0.4051
res_gsdis  4 145.75 156.29 -68.874   137.75      2    0.4051
>
> #Including results in AIC list
> models[[3]]<-res_gsdis
> Modnames <- rbind(Modnames, "Group size and distance to core area model")
>
>
> #Calculating R2
> r2_gsdis<-r.squaredGLMM(res_gsdis)
Error in glmer(formula = winner_analysis ~ rel_groupsize + rel_distancetocorearea + :
  fitting model with the observation-level random effect term failed. Add the term manually
In addition: warning message:
In value[[3L]](cond) : (p <- ncol(X)) == ncol(Y) is not TRUE
>
> R2<-rbind(R2,r2_gsdis)
>
>
> #Probability plot
> plotLMER.fnc(res_gsdis,ylimit=0:1,lockYlim=TRUE,linecolor="red",
+             lwd=4,xlabel="Relative group size",
+             ylabel="Probability of winning")
log odds are back-transformed to probabilities
effect size (range) for rel_groupsize is 0.06449084
effect size (range) for rel_distancetocorearea is 0.4306809
```





```
> #####
#####
>
> cat("\n\n\n\n\n RESULTS\n\n\n\n\n")
```

RESULTS

```
>
> #####
#####
> ## Best model according to AIC
>
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TR
UE)
```

Model selection based on AICC:

	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
Null model	2	143.68	0.00	0.48	0.48	-69.78
Group size and use of space model	4	144.19	0.51	0.38	0.86	-67.89
Group size and distance to core area model	4	146.16	2.48	0.14	1.00	-68.87

Warning message:

```
In data.row.names(row.names, rowsi, i) :
  some row.names duplicated: 3 --> row.names NOT used
```

```
>
> ## Best model according to R2
> R2
      R2m      R2c
R2      0.00000000 0.008077611
r2_gsud 0.04591970 0.057570373
r2_gsdis 0.01354437 0.021484504
>
>
>
```



```

>
> cat("\n\n What variability does dyad2 explain? \n\n")

What variability does dyad2 explain?

>
>
> res_dy=glm(winner_analysis ~ dyad2, family="binomial", data=factors_original)
> res.nulldy=glm(winner_analysis ~ 1, family="binomial", data=factors_original)
>
> print(summary(res_dy))

Call:
glm(formula = winner_analysis ~ dyad2, family = "binomial", data = factors_original)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6006  -1.1483   0.8067   1.0579   1.5645

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.06899    0.37161  -0.186  0.8527
dyad2r1pb1   1.02450    0.52589   1.948  0.0514 .
dyad2r1r2   -0.80648    0.64918  -1.242  0.2141
dyad2r2r1    0.35667    0.57666   0.619  0.5362
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 141.61  on 102  degrees of freedom
Residual deviance: 131.99  on  99  degrees of freedom
(1 observation deleted due to missingness)
AIC: 139.99

Number of Fisher Scoring iterations: 4

>
> cat("\n\n Comparison between dyad2 model and null model\n\n")

Comparison between dyad2 model and null model

>
> print(anova(res.nulldy,res_dy, test="Chisq"))
Analysis of Deviance Table

Model 1: winner_analysis ~ 1
Model 2: winner_analysis ~ dyad2
  Resid. Df Resid. Dev Df Deviance Pr(>Chi)
1        102      141.61
2         99      131.99  3    9.6234  0.02205 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> summary(res_dy)

```

```

Call:
glm(formula = winner_analysis ~ dyad2, family = "binomial", data = factors_original)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6006  -1.1483   0.8067   1.0579   1.5645

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.06899    0.37161  -0.186   0.8527
dyad2r1pb1   1.02450    0.52589   1.948   0.0514 .
dyad2r1r2   -0.80648    0.64918  -1.242   0.2141
dyad2r2r1    0.35667    0.57666   0.619   0.5362
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 141.61  on 102  degrees of freedom
Residual deviance: 131.99  on  99  degrees of freedom
(1 observation deleted due to missingness)
AIC: 139.99

Number of Fisher Scoring iterations: 4

>
>
> #Calculate (pseudo) R-squared statistics
>
> RsqGLM(res_dy)
$CoxSnell
[1] 0.08919898

$Nagelkerke
[1] 0.1193893

$McFadden
[1] 0.06795625

$Tjur
[1] 0.09115383

$sqPearson
[1] 0.09115383

```

CHAPTER 3: SUPPLEMENTARY INFORMATION

3.1. R Scripts of models predicting the probability of intergroup outcome and intensity in crested macaques considering reproductive strategies

3.1.1. MODELS PREDICTING THE PROBABILITY OF DECIDED INTERGROUP ENCOUNTER

```
## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr
```

```
# using the package:
updateR() # This will start the updating process of your R installation.
# It will check for newer versions, and if one is available, will guide you through the decisions you'd need to make.
```

```
## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("ppcor")#To check for correlations between independent variables
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine

library(lme4)
library(car)
library(ggplot2)
```

```
## Upload data
factors_original<-read.csv("factors_originalv1.csv")
```

```
#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison
cannot be made)
missingrows = is.na(factors_original$ abs_nummales)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numfemales)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numinfperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numinfpermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_swfemperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_swfempermale)
factors_original= factors_original[!missingrows,]
```

```
missingrows = is.na(factors_original$abs_sexratio)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$decided_undecided)#The outcome of all IGEs was known, so this is just a
formality
factors_original= factors_original[!missingrows,]

cat("\n\n\n Checking correlations between fixed effects (before eliminating ) \n\n\n")

#Correlations between variables for the female-based models
fdata<-
data.frame(factors_original$abs_numfemales,factors_original$abs_numinfperfem,factors_original$abs_swfem
perfem,factors_original$abs_sexratio)
pcor(fdata)

#Correlations between variables for the male-based models
mdata<-
data.frame(factors_original$abs_nummales,factors_original$abs_numinfpermale,factors_original$abs_swfemp
ermale,factors_original$abs_sexratio)
pcor(mdata)

cat("\n\n\n\n\n\n\n Checking potential control variables \n\n\n\n\n\n\n")
#Same as in the models with group size and location only

resdu_cv=glmer(decided_undecided ~ 1+durationIGE+num_obs+ (1|dyad), family="binomial",
data=factors_original)

print(summary(resdu_cv))

#Comparison between the null model and the model with the potential c.variables
resdu.null=glmer(decided_undecided ~ 1 +(1|dyad), family="binomial", data=factors_original)
print(anova(resdu.null,resdu_cv, test="Chisq"))
#Not significant, they won't be considered.

#Starting a list to calculate AICs to compare between all the models
models<-list()
models[[1]]<-resdu.null
Modnames <- "Null model"

#Calculating R2
r2_null<-r.squaredGLMM(resdu.null)

R2_und<-r2_null

#Checking how many dyads are left in the data
table(factors_original$decided_undecided,
      factors_original$dyad)
```



```

(1|dyad), family="binomial", data=factors_original)

print(summary(resdu_fcc))

#Including model in AIC list
models[[4]]<-resdu_fcc
Modnames<-rbind(Modnames, "Full female (cat.core) model")

#Calculating R2

r2_fullfem_coreyn<-r.squaredGLMM(resdu_fcc)
R2_und<-rbind(R2_und,r2_fullfem_coreyn)

cat("\n\n\n Comparison of female based model (full) to null model\n\n")
print(anova(resdu.null,resdu_fcc, test="Chisq"))

#Although n.females was the only significant factor; since the full model was not significantly different from the
null model
# no adjusted model is run

cat("\n\n\n\n\n\n\n Male based model \n\n\n\n\n\n\n\n")

cat("\n\n\n\n\n Intensity of use of space\n\n\n\n\n\n")
# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Control variable/s: none
# Fixed effects: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190
# Random effect: 'dyad', 3 levels.
# Hypothesis: Odds of a draw would be higher (1) when the number of males are similar, (2) when the
proportion of infants/male are similar
# (3) when the proportion of fertile females/male are similar (4) when the sex ratios (f:m) are similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190, family="binomial",
data=factors_original))
# abs_sexratio displays values of vif higher than 3 (threshold recommended in Zuur et al. 2010), so it will be
dropped
vif(glm(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190,
family="binomial", data=factors_original))
#The second with higher vif is abs_numinfpermale. If by dropping it we can lower the vif of sex ratio, I can ran 2
sets of model, each starting with one of the 2 dropped variables
vif(glm(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+abs_UD190, family="binomial",
data=factors_original))

#Run model (no sex ratio)
resdu_miu1=glmer(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190+
(1|dyad), family="binomial", data=factors_original)

print(summary(resdu_miu1))

```



```
plotLMER.fnc(resdu_miu1,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of decided encounter")

cat("\n\n\n Comparison of male based model (full, no sex ratio) to null model\n\n")
print(anova(resdu.null,resdu_miu1, test="Chisq"))
#Fullmodel significantly different from null model and 2 fixed factors significant. Adjusted model with such
factors is produced

#Including model in AIC list
models[[5]]<-resdu_miu1

subset<-list()
subset[[1]]<-resdu_miu1
Modnames<-rbind(Modnames, "Full male (i.u, no sex ratio) model")

#Calculating R2

r2_fullmal_iu1<-r.squaredGLMM(resdu_miu1)
R2_und<-rbind(R2_und,r2_fullmal_iu1)

#Run model (adjusted:no.males+pr.infants)
resdu_m=glmer(decided_undecided ~ abs_nummales+abs_numinfpermale+
              (1|dyad), family="binomial", data=factors_original)

print(summary(resdu_m))

cat("\n\n\n Comparison of male based model (no.males+pr.infants) to null model\n\n")
print(anova(resdu.null,resdu_m,est="Chisq"))

plotLMER.fnc(resdu_m,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of decided encounter")

#Including model in AIC list
models[[6]]<-resdu_m
subset[[2]]<-resdu_m
Modnames<-rbind(Modnames, "No.males+pr.infants model")

#Calculating R2

r2_m<-r.squaredGLMM(resdu_m)
R2_und<-rbind(R2_und,r2_m)

#Run model (full without proportion of infants)
resdu_miu2=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+abs_UD190+
                 (1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resdu_miu2))

cat("\n\n\n Comparison of male based model (full without pr.infants) to null model\n\n")
print(anova(resdu.null,resdu_miu2, test="Chisq"))
#Fullmodel significantly different from null model and 2 fixed factors significant. Adjusted model with such
factors is produced

plotLMER.fnc(resdu_miu2,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of decided encounter")

#Including model in AIC list
models[[7]]<-resdu_miu2
subset[[3]]<-resdu_miu2
Modnames<-rbind(Modnames, "Full male (i.u, no pr.infants) model")

#Calculating R2

r2_fullmal_iu2<-r.squaredGLMM(resdu_miu2)
R2_und<-rbind(R2_und,r2_fullmal_iu2)

#Run model (adjusted from full male model without pr.infants)
resdu_m2=glmer(decided_undecided ~ abs_nummales+abs_sexratio+
              (1|dyad), family="binomial", data=factors_original)

print(summary(resdu_m2))

cat("\n\n\n Comparison of male based model (no.males+sex.ratio) to null model\n\n")
print(anova(resdu.null,resdu_m2,est="Chisq"))

plotLMER.fnc(resdu_m2,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of decided encounter")

#Including model in AIC list
models[[8]]<-resdu_m2
subset[[4]]<-resdu_m2
Modnames<-rbind(Modnames, "Male (adj. no.males+sex.ratio)model")

#Calculating R2

r2_m2<-r.squaredGLMM(resdu_m2)
R2_und<-rbind(R2_und,r2_m2)

cat("\n\n\n\n Absolute distance to core\n\n\n\n\n")
```

```

# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
# Control variable/s: none
# Fixed effects: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea
# Random effect: 'dyad', 3 levels.
# Hypothesis: Odds of a draw would be higher (1) when the number of males are similar, (2) when the
proportion of infants/male are similar
# (3) when the proportion of fertile females/male are similar (4) when the sex ratios (f:m) are similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea,
family="binomial", data=factors_original))
#Same problem as the previous set of models. Now without sex ratio
vif(glm(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea, family="binomial",
data=factors_original))
#and without pr. infants
vif(glm(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea,
family="binomial", data=factors_original))

#Run full model (no sex ratio)

resdu_mdc1=glmer(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea+
(1|dyad), family="binomial", data=factors_original)

print(summary(resdu_mdc1))

cat("\n\n\n Comparison of male based model (full) to null model\n\n")
print(anova(resdu.null,resdu_mdc1, test="Chisq"))
#An adjusted model will be done with pr.infants per male only

plotLMER.fnc(resdu_mdc1,ylimit=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,
ylabel="Probability of decided encounter")

#Including model in AIC list
models[[9]]<-resdu_mdc1
Modnames<-rbind(Modnames, "Full male (d.c., no sex ratio)model")

#Calculating R2

r2_fullmal_dc1<-r.squaredGLMM(resdu_mdc1)
R2_und<-rbind(R2_und,r2_fullmal_dc1)

#Run adjusted model (no sex ratio)

resdu_m3=glmer(decided_undecided ~ abs_numinfpermale+
(1|dyad), family="binomial", data=factors_original)

```

```
print(summary(resdu_m3))

plotLMER.fnc(resdu_m3,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of decided encounter")

cat("\n\n\n Comparison of male based model (only prop.infants per male) to null model\n\n")
print(anova(resdu.null,resdu_m3, test="Chisq"))

#Including model in AIC list
models[[10]]<-resdu_m3
Modnames<-rbind(Modnames, "Pr.infants per male model")

#Calculating R2

r2_m3<-r.squaredGLMM(resdu_m3)
R2_und<-rbind(R2_und,r2_m3)

#Run full model (no prop.infants)

resdu_mdc2=glmer(decided_undecided ~
abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea+
              (1|dyad), family="binomial", data=factors_original)

print(summary(resdu_mdc2))

cat("\n\n\n Comparison of male based model (full, no pr.infants) to null model\n\n")
print(anova(resdu.null,resdu_mdc2, test="Chisq"))
#An adjusted model would apply with No.males+sex ratio, but was done previously when the full model
included i.u instead of distance to core

plotLMER.fnc(resdu_mdc2,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of decided encounter")

#Including model in AIC list
models[[11]]<-resdu_mdc2
subset[[5]]<-resdu_mdc2
Modnames<-rbind(Modnames, "Full male (d.c., no pr.infants)model ")

#Calculating R2

r2_fullmal_dc2<-r.squaredGLMM(resdu_mdc2)
R2_und<-rbind(R2_und,r2_fullmal_dc2)

cat("\n\n\n\n Categorical core area\n\n\n\n\n\n")

# Response: decided_undecided (binary,1=Decided IGE, 0=Undecided IGE)
```

```
# Control variable/s: none
# Fixed effects: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# Hypothesis: Odds of a draw would be higher (1) when the number of males are similar, (2) when the
proportion of infants/male are similar
# (3) when the proportion of fertile females/male are similar (4) when the sex ratios (f:m) are similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn,
family="binomial", data=factors_original))
#Same thing again
vif(glm(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn,
family="binomial", data=factors_original))
vif(glm(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+core_yn, family="binomial",
data=factors_original))

#Run the full model model (no sex ratio)

resdu_mcc1=glmer(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+
(1|dyad), family="binomial", data=factors_original)

print(summary(resdu_mcc1))

plotLMER.fnc(resdu_mcc1,ylimit=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,
ylabel="Probability of decided encounter")

cat("\n\n\n Comparison of male based model (full) to null model\n\n")
print(anova(resdu.null,resdu_mcc1, test="Chisq"))
#Adjusted model would no.males+pr.infants, which has already been included

#Including model in AIC list
models[[12]]<-resdu_mcc1
subset[[6]]<-resdu_mcc1
Modnames<-rbind(Modnames, "Full male (c.c., no sex ratio) model")

#Calculating R2

r2_fullmal_cc1<-r.squaredGLMM(resdu_mcc1)
R2_und<-rbind(R2_und,r2_fullmal_cc1)

#Run the full model model (no pr.infants)

resdu_mcc2=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+core_yn+
(1|dyad), family="binomial", data=factors_original)

print(summary(resdu_mcc2))
```

```

cat("\n\n Comparison of male based model (full) to null model\n\n")
print(anova(resdu.null,resdu_mcc2, test="Chisq"))
#Adjusted model would no.males+abs sex ratio, which has already been included

plotLMER.fnc(resdu_mcc2,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,
             ylabel="Probability of decided encounter")

#Including model in AIC list
models[[13]]<-resdu_mcc2
subset[[7]]<-resdu_mcc2
Modnames<-rbind(Modnames, "Full male (c.c., no pr.infants) model")

#Calculating R2

r2_fullmal_cc2<-r.squaredGLMM(resdu_mcc2)
R2_und<-rbind(R2_und,r2_fullmal_cc2)

#####
#####
#####
#####
####          SUMMARY OF RESULTS 1 (with all the database)          #####
####          #####
#####
#####

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
#Male models with some measurement of distance are the most explanatory

R2_und

#Evidence ratios
aictab<-aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictab, model.high = "top", model.low = "second.ranked")
evidence(aictab, model.high = "top", model.low = "Male (adj. no.males+sex.ratio)model")
evidence(aictab, model.high = "top", model.low = "Full male (c.c., no sex ratio) model")
evidence(aictab, model.high = "top", model.low = "Full male (i.u, no pr.infants) model")
evidence(aictab, model.high = "top", model.low = "Full male (i.u, no sex ratio) model")
evidence(aictab, model.high = "top", model.low = "Full male (d.c., no pr.infants)model")
evidence(aictab, model.high = "top", model.low = "Full male (d.c., no sex ratio)model")
evidence(aictab, model.high = "top", model.low = "Pr.infants per male model")
evidence(aictab, model.high = "top", model.low = "Null model")
evidence(aictab, model.high = "top", model.low = "Full female (l.U) model")

```

```
evidence(aictab, model.high = "top", model.low = "Full female (cat.core) model")

topmodels<-get.models(models, subset=delta<2)

#Model averaging
#First we generate an "averaging" object by averaging the full range of models and then being able to select the
#top models with the function get.models
# instead of having to do it manually.

av<-(model.avg(models, beta = c("none", "sd", "partial.sd")))
topmodels<-get.models(av, subset=delta<2)
summary(model.avg(topmodels, beta = c("none", "sd", "partial.sd")))

##The 'subset' (or 'conditional') average only averages over the models where the parameter appears.
#An alternative, the 'full' average assumes that a variable is included in every model, but in some
#models the corresponding coefficient (and its respective variance) is set to zero. Unlike the 'subset
#average', it does not have a tendency of biasing the value away from zero. The 'full' average is
#a type of shrinkage estimator and for variables with a weak relationship to the response they are" (From
Barton 2017, p.35)
#smaller than 'subset' estimators.
confint(model.avg(topmodels, beta = c("none", "sd", "partial.sd")))

#Manual subsetting Only including the subset of models that had a deltaAICc<2
summary(model.avg(subset, beta = c("none", "sd", "partial.sd")))

#Graphs of the best model of the series

sjp.glmer(resdu_mcc1, type="pred", facet.grid=FALSE, vars="abs_nummales",geom.colors =
"bw",show.ci=TRUE)

sjp.glmer(resdu_mcc1, type="pred", facet.grid=FALSE, vars="abs_numinfpermale",geom.colors =
"bw",show.ci=TRUE)

sjp.glmer(resdu_mcc1, type="pred", facet.grid=FALSE, vars="abs_swfempermale",geom.colors =
"bw",show.ci=TRUE)

sjp.glmer(resdu_mcc2, type="pred", facet.grid=FALSE, vars="abs_sexratio",geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resdu_mcc1, type="pred", facet.grid=FALSE, vars="core_yn",geom.colors = "bw",show.ci=TRUE)

##The other location factors in the next best models
sjp.glmer(resdu_mdc1, type="pred", facet.grid=FALSE, vars="abs_distancetocorearea",geom.colors =
"bw",show.ci=TRUE)

sjp.glmer(resdu_miu1, type="pred", facet.grid=FALSE, vars="abs_UD190",geom.colors = "bw",show.ci=TRUE)

cat("\n\n\n\n Comparison with the best model of the previous chapter (Group size)\n\n\n\n\n")
```

####Note that since the sample sizes are different due to the lack of some infant & swelling data, the AICs and R2 shouldn't be directly compared between chapters. Because of this, I recalculate the model here with the current sample to allow for an appropriate comparison

#Formating the variable

```
factors_original$abs_groupsize<- as.numeric(factors_original$abs_groupsize)
```

#Creating the group size (the best model of the previous chapter)

```
resdu_gs=glmer(decided_undecided ~ abs_groupsize+(1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resdu_gs))
```

```
cat("\n\n\n Comparison of group size model to null model\n\n")
```

```
print(anova(resdu.null,resdu_gs, test="Chisq"))
```

#Including model in AIC list

```
models[[14]]<-resdu_gs
```

```
Modnames<-rbind(Modnames, "Group size model")
```

#Calculating R2

```
r2_gs<-r.squaredGLMM(resdu_gs)
```

```
R2_und<-rbind(R2_und,r2_gs)
```

```
cat("\n\n\n\n\n Is the model of the previous chapter better than the best one of this one?\n\n\n\n\n")
```

```
aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
```

```
R2_und
```

#Evidence ratio

```
aictab<-aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
```

```
evidence(aictab, model.high = "top", model.low = "second.ranked")
```

```
evidence(aictab, model.high = "top", model.low = "Male (adj. no.males+sex.ratio)model")
```

```
evidence(aictab, model.high = "top", model.low = "Full male (c.c., no sex ratio) model")
```

```
evidence(aictab, model.high = "top", model.low = "Group size model")
```

```
evidence(aictab, model.high = "top", model.low = "Full male (i.u, no pr.infants) model")
```

```
evidence(aictab, model.high = "top", model.low = "Full male (i.u, no sex ratio) model")
```

```
evidence(aictab, model.high = "top", model.low = "Full male (d.c., no pr.infants)model ")
```

```
evidence(aictab, model.high = "top", model.low = "Full male (d.c., no sex ratio)model")
```

```
evidence(aictab, model.high = "top", model.low = "Pr.infants per male model")
```

```
evidence(aictab, model.high = "top", model.low = "Null model")
```

```
evidence(aictab, model.high = "top", model.low = "Full female (I.U) model")
```

```
evidence(aictab, model.high = "top", model.low = "Full female (cat.core) model")
```

#No, some male models are better, although this one is comparably good (within 2 AICc)


```
sjp.glmer(resdu_gs, type="pred", facet.grid=FALSE, vars="abs_groupsize",geom.colors = "bw",show.ci=TRUE)
```

```
cat("\n\n\n\n\n\n\n\n\n\n What if we retain only those variables that are common in the models with a evidence  
ratio <2? \n\n\n\n\n\n\n\n\n\n")
```

```
#Creating the abs_nummales+abs_swfempermale model
```

```
vif(glm(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale, family="binomial",  
data=factors_original))
```

```
resdu_m=glmer(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+(1|dyad),  
family="binomial", data=factors_original)
```

```
print(summary(resdu_m))
```

```
cat("\n\n\n Comparison of male red. model to null model\n\n")  
print(anova(resdu.null,resdu_m, test="Chisq"))
```

```
#Including model in AIC list  
models[[15]]<-resdu_m  
Modnames<-rbind(Modnames, "Red.male model")
```

```
#Calculating R2
```

```
r2_m<-r.squaredGLMM(resdu_m)  
R2_und<-rbind(R2_und,r2_m)
```

```
aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)  
R2_und  
aictab<-aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)  
evidence(aictab, model.high = "top", model.low = "second.ranked")
```

```
cat("\n\n\n Calculating effective sizes of the three strongest fixed factors together \n\n")
```

```
resdu_bff=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+(1|dyad),  
family="binomial", data=factors_original)
```

```
print(summary(resdu_bff))
```

```
plotLMER.fnc(resdu_bff,ylim=0:1,lockYlim=TRUE,linecolor="red",  
lwd=4,  
ylabel="Probability of decided encounter")
```

```
#####
#####
#####

cat("\n\n\n\n\n\n\n\n\n\n What happens if we remove the 2 IGE pb1-r2? \n\n\n\n\n\n\n\n\n\n")

#####
###
#####
###

nopb1r2<-factors_original[factors_original$dyad!="pb1r2",]
resdu.null2=glmer(decided_undecided ~ 1+ (1|dyad), family="binomial", data=nopb1r2)
print(summary(resdu.null2))

#Starting a list to calculate AICs to compare between all the models
models2<-list()
models2[[1]]<-resdu.null2
Modnames2 <- "Null model (nopb1r2)"

#Calculating R2
r2_null2<-r.squaredGLMM(resdu.null2)

R2_und2<-r2_null2

cat("\n\n\n\n\n\n\n\n\n\n Female-based models2 \n\n\n\n\n\n\n\n\n\n")

cat("\n\n\n\n\n\n\n\n\n\n Absolute intensity of use of space \n\n\n\n\n\n\n\n\n\n")

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190, family="binomial",
data=nopb1r2))

#Run the model

resdu_fiu2=glmer(decided_undecided ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190+
(1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_fiu2))

#Including model in AIC list
models2[[2]]<-resdu_fiu2
Modnames2<-rbind(Modnames2, "Full female (I.U) model2")
```

```
#Calculating R2
```

```
r2_fullfem_iu2<-r.squaredGLMM(resdu_fiu2)
R2_und2<-rbind(R2_und2,r2_fullfem_iu2)
```

```
cat("\n\n\n Comparison of female based model (full) to null model\n\n")
print(anova(resdu.null2,resdu_fiu2, test="Chisq"))
```

#Since the full model is not significantly different from the null model, no adjusted model with the only sign.factor is performed.

```
cat("\n\n\n\n\n\n\n\n Absolute distance to core \n\n\n\n\n\n\n\n\n\n")
```

```
#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea,
family="binomial", data=nopb1r2))
```

```
#Run the model
```

```
resdu_fdc2=glmer(decided_undecided ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea+
(1|dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resdu_fdc2))
```

```
#Including model in AIC list
models2[[3]]<-resdu_fdc2
Modnames2<-rbind(Modnames2, "Full female (D.C.) model 2")
```

```
#Calculating R2
```

```
r2_fullfem_dc2<-r.squaredGLMM(resdu_fdc2)
R2_und2<-rbind(R2_und2,r2_fullfem_dc2)
```

```
cat("\n\n\n\n Comparison of female based model (full) to null model\n\n")
print(anova(resdu.null2,resdu_fdc2, test="Chisq"))
```

```
cat("\n\n\n\n\n\n\n\n\n\n Categorical core area \n\n\n\n\n\n\n\n\n\n")
```

```
#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~ abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn,
family="binomial", data=nopb1r2))
```

```
#Run the model
```

```
resdu_fcc2=glmer(decided_undecided ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn+
(1|dyad), family="binomial", data=nopb1r2)
```



```
Modnames2<-rbind(Modnames2, "Full male (i.u, no sex ratio) model 2")

#Calculating R2

r2_fullmal_iu12<-r.squaredGLMM(resdu_miu12)
R2_und2<-rbind(R2_und2,r2_fullmal_iu1)


#Run model (full without proportion of infants)
resdu_miu22=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+abs_UD190+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_miu22))

cat("\n\n\n Comparison of male based model (full without pr.infants) to null model\n\n")
print(anova(resdu.null2,resdu_miu22, test="Chisq"))
#Fullmodel not significantly different from null model


#Including model in AIC list
models2[[6]]<-resdu_miu22
Modnames2<-rbind(Modnames2, "Full male (i.u, no pr.infants) model 2")

#Calculating R2

r2_fullmal_iu22<-r.squaredGLMM(resdu_miu22)
R2_und2<-rbind(R2_und2,r2_fullmal_iu22)


cat("\n\n\n\nAbsolute distance to core\n\n\n\n\n")

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea,
family="binomial", data=nopb1r2))
#Same problem as the previous set of models2. Now without sex ratio
vif(glm(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea, family="binomial",
data=nopb1r2))
#and without pr. infants
vif(glm(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea,
family="binomial", data=nopb1r2))


#Run full model (no sex ratio)
resdu_mdc12=glmer(decided_undecided ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_mdc12))
```

```
cat("\n\n\n Comparison of male based model (full) to null model\n\n")
print(anova(resdu.null2,resdu_mdc12, test="Chisq"))

#Including model in AIC list
models2[[7]]<-resdu_mdc12
Modnames2<-rbind(Modnames2, "Full male (d.c., no sex ratio)model 2")

#Calculating R2

r2_fullmal_dc12<-r.squaredGLMM(resdu_mdc12)
R2_und2<-rbind(R2_und2,r2_fullmal_dc12)

#Run full model (no prop.infants)

resdu_mdc22=glmer(decided_undecided ~
abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea+
(1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_mdc22))

cat("\n\n\n Comparison of male based model (full, no pr.infants) to null model\n\n")
print(anova(resdu.null2,resdu_mdc22, test="Chisq"))

#Including model in AIC list
models2[[8]]<-resdu_mdc22
Modnames2<-rbind(Modnames2, "Full male (d.c., no pr.infants)model 2")

#Calculating R2

r2_fullmal_dc22<-r.squaredGLMM(resdu_mdc22)
R2_und2<-rbind(R2_und2,r2_fullmal_dc22)

cat("\n\n\n\n Categorical core area\n\n\n\n\n")

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn,
family="binomial", data=nopb1r2))
#Same thing again
vif(glm(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn,
family="binomial", data=nopb1r2))
vif(glm(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+core_yn, family="binomial",
data=nopb1r2))

#Run the full model model (no sex ratio)

resdu_mcc12=glmer(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+
(1|dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resdu_mcc12))

cat("\n\n\n Comparison of male based model (full) to null model\n\n")
print(anova(resdu.null2,resdu_mcc12, test="Chisq"))

#Including model in AIC list
models2[[9]]<-resdu_mcc12
Modnames2<-rbind(Modnames2, "Full male (c.c., no sex ratio) model 2")

#Calculating R2

r2_fullmal_cc12<-r.squaredGLMM(resdu_mcc12)
R2_und2<-rbind(R2_und2,r2_fullmal_cc12)

#Run the full model model (no pr.infants)

resdu_mcc22=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+core_yn+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_mcc22))

cat("\n\n\n Comparison of male based model (full) to null model\n\n")
print(anova(resdu.null2,resdu_mcc22, test="Chisq"))
#Adjusted model needed

#Including model in AIC list
models2[[10]]<-resdu_mcc22
Modnames2<-rbind(Modnames2, "Full male (c.c., no pr.infants) model 2")

#Calculating R2

r2_fullmal_cc22<-r.squaredGLMM(resdu_mcc22)
R2_und2<-rbind(R2_und2,r2_fullmal_cc22)

#Run adj model (sex ratio only)

resdu_sr=glmer(decided_undecided ~ abs_sexratio+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resdu_sr))

cat("\n\n\n Comparison of sexratio to null model\n\n")
print(anova(resdu.null2,resdu_sr, test="Chisq"))

#Including model in AIC list
```

```

models2[[11]]<-resdu_sr
Modnames2<-rbind(Modnames2, "Sex ratio model 2")

#Calculating R2

r2_sr<-r.squaredGLMM(resdu_sr)
R2_und2<-rbind(R2_und2,r2_sr)

#####
#####
#####
#####
####              SUMMARY OF RESULTS 2 (nopb1r2)              #####
####              #####
#####
#####

aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
aictab<-aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictab, model.high = "top", model.low = "second.ranked")
evidence(aictab, model.high = "top", model.low = "Full male (i.u, no sex ratio) model")
evidence(aictab, model.high = "top", model.low = "Full male (c.c., no pr.infants) model 2")
evidence(aictab, model.high = "top", model.low = "Null model (nopb1r2)")
evidence(aictab, model.high = "top", model.low = "Full male (c.c., no sex ratio) model 2")
evidence(aictab, model.high = "top", model.low = "Full male (d.c., no pr.infants)model 2")
evidence(aictab, model.high = "top", model.low = "Full male (d.c., no sex ratio)model 2")
evidence(aictab, model.high = "top", model.low = "Full female (I.U) model2")
evidence(aictab, model.high = "top", model.low = "Full female (D.C.), model 2")
evidence(aictab, model.high = "top", model.low = "Full female (cat.core) model 2")

R2_und2

#Model averaging

av2<-(model.avg(models2, beta = c("none", "sd", "partial.sd")))
topmodels2<-get.models(av2, subset=delta<2)
summary(model.avg(topmodels2, beta = c("none", "sd", "partial.sd")))

confint((model.avg(topmodels2, beta = c("none", "sd", "partial.sd"))))

#The best model is the sex ratio model followed by null

sjp.glmer(resdu_mcc22, type="pred", facet.grid=FALSE, vars="abs_nummales",geom.colors =
"bw",show.ci=TRUE)

sjp.glmer(resdu_mcc12, type="pred", facet.grid=FALSE, vars="abs_numinfpermale",geom.colors =
"bw",show.ci=TRUE)

sjp.glmer(resdu_mcc22, type="pred", facet.grid=FALSE, vars="abs_swfempermale",geom.colors =
"bw",show.ci=TRUE)

sjp.glmer(resdu_mcc22, type="pred", facet.grid=FALSE, vars="abs_sexratio",geom.colors = "bw",show.ci=TRUE)

sjp.glmer(resdu_miu22, type="pred", facet.grid=FALSE, vars="abs_UD190",geom.colors = "bw",show.ci=TRUE)

```



```
sjp.glmer(resdu_mdc22, type="pred", facet.grid=FALSE, vars="abs_distancetocorearea",geom.colors =  
"bw",show.ci=TRUE)
```

```
sjp.glmer(resdu_mcc22, type="pred", facet.grid=FALSE, vars="core_yn",geom.colors = "bw",show.ci=TRUE)
```

```
cat("\n\n\n\n Comparison with the best model of the previous chapter (Group size ) without  
pb1r2\n\n\n\n\n")
```

```
####Note that since the sample sizes are different due to the lack of some infant & swelling data, the AICs and R2  
shouldn't be directly
```

```
####compared between chapters. Because of this, I recalculate the model here with the current sample to allow  
for an appropriate comparison
```

```
#Formating the variable
```

```
nopb1r2$abs_groupsize<- as.numeric(nopb1r2$abs_groupsize)
```

```
#Creating the group size (the best model of the previous chapter)
```

```
resdu_gs2=glmer(decided_undecided ~ abs_groupsize+(1|dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resdu_gs2))
```

```
cat("\n\n\n Comparison of group size to null model\n\n")
```

```
print(anova(resdu.null2,resdu_gs2, test="Chisq"))
```

```
#Including model in AIC list
```

```
models2[[12]]<-resdu_gs
```

```
Modnames2<-rbind(Modnames2, "g.size model 2")
```

```
#Calculating R2
```

```
r2_gs2<-r.squaredGLMM(resdu_gs2)
```

```
R2_und2<-rbind(R2_und2,r2_gs2)
```

```
cat("\n\n\n\n\n Is the model of the previous chapter better than the best one of this one?\n\n\n\n\n")
```

```
aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
```

```
R2_und2
```

```
aictab<-aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
```

```
evidence(aictab, model.high = "top", model.low = "g.size model 2")
```

```
sjp.glmer(resdu_gs2, type="pred", facet.grid=FALSE, vars="abs_groupsize",geom.colors = "bw",show.ci=TRUE)
```

```
cat("\n\nCalculating effective sizes of the three strongest fixed factors together\n\n")

resdu_bff2=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_sexratio+(1|dyad),
family="binomial", data=nopb1r2)

print(summary(resdu_bff2))

plotLMER.fnc(resdu_bff2,ylim=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,
ylabel="Probability of decided encounter")

#####
#####
#####
#####
#####
#####
cat("\n\n\n\n\n Post-hoc exploration\n\n\n\n\n")

# The patterns show that when No. males are similar, draws are more likely. If the groups differ in proportion of
tumescant females,
# Pr.infants per male and sex ratio, then the encounters tend to be undecided.
# I hypothesize that the negative correlated factors might regulate the the realized RHP in a way that makes is
similar in both group,
# leading to higher draw chances. This may happen in smaller groups tend to have higher prop. infants (more
intergroup aggression
# expected by males as a "hired guns"); lower pr. of tumescant females (which would decrease herding and
increase intergroup aggression)
# and lower sex ratio (less mating skew, more males interested in defending potential offspring and mating
opportunities)

trial=glmer(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_nummales*abs_numinfpermale+
(1|dyad), family="binomial", data=factors_original)

print(summary(trial))

trial2=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_nummales*abs_swfempermale+
(1|dyad), family="binomial", data=factors_original)

print(summary(trial2))#This is the only interaction almost significant

trial3=glmer(decided_undecided ~ abs_nummales+abs_sexratio+abs_nummales*abs_sexratio+
(1|dyad), family="binomial", data=factors_original)

print(summary(trial3))
```

```
##No pb1-r2

trial4=glmer(decided_undecided ~ abs_nummales+abs_numinfpermale+abs_nummales*abs_numinfpermale+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(trial4))

trial5=glmer(decided_undecided ~ abs_nummales+abs_swfempermale+abs_nummales*abs_swfempermale+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(trial5))

trial6=glmer(decided_undecided ~ abs_nummales+abs_sexratio+abs_nummales*abs_sexratio+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(trial6))#This is the only interaction almost significant


## Upload data
demo_groups<-read.csv("IGE_demographicdata.csv")

pb1<-demo_groups[demo_groups$GROUP=="PB1",]
r1<-demo_groups[demo_groups$GROUP=="R1",]
r2<-demo_groups[demo_groups$GROUP=="R2",]

install.packages("ppcor")
library(ppcor)

summary(pb1)
pb1d<-data.frame(pb1$N_males, pb1$PrInfMale,pb1$PrTumMale, pb1$sexratio)
pb1d<-na.omit(pb1d)
pcor(pb1d)

summary(r1)
r1d<-data.frame(r1$N_males, r1$PrInfMale,r1$PrTumMale, r1$sexratio)
r1d<-na.omit(r1d)
pcor(r1d)

summary(r2)

r2d<-data.frame(r2$N_males, r2$PrInfMale,r2$PrTumMale, r2$sexratio)
r2d<-na.omit(r2d)
pcor(r2d)

boxplot(N_males~ GROUP,
  data = demo_groups, xlab="Group", ylab="No.Males")

p<-ggplot(demo_groups,aes(GROUP, N_males))
```

```
p+ geom_boxplot()+  
  geom_jitter(width = 0.2)+  
  labs(x = "Group", y="No.Males")+  
  theme_bw()
```

```
boxplot(PrInfMale~ GROUP,  
  data = demo_groups, xlab="Group", ylab="Infants per male")
```

```
p<-ggplot(demo_groups,aes(GROUP, PrInfMale))  
p+ geom_boxplot()+  
  geom_jitter(width = 0.2)+  
  labs(x = "Group", y="Infants per male")+  
  theme_bw()
```

```
boxplot(sexratio~ GROUP,  
  data = demo_groups,xlab="Group", ylab="Sex ratio (f:m)")
```

```
p<-ggplot(demo_groups,aes(GROUP, sexratio))  
p+ geom_boxplot()+  
  geom_jitter(width = 0.2)+  
  labs(x = "Group", y="Females per male")+  
  theme_bw()
```

```
boxplot(PrTumMale~ GROUP,  
  data = demo_groups, xlab="Group", ylab="Tumescent females per male")
```

```
p<-ggplot(demo_groups,aes(GROUP, PrTumMale))  
p+ geom_boxplot()+  
  geom_jitter(width = 0.2)+  
  labs(x = "Group", y="Tumescent females per male")+  
  theme_bw()
```

3.1.2. MODELS PREDICTING THE PROBABILITY OF WINING AN ENCOUNTER

```
## download packages  
# installing/loading the package:  
if(!require(installr)) {  
  install.packages("installr"); require(installr)} #load / install+load installr  
  
# using the package:  
updateR() # This will start the updating process of your R installation.  
# It will check for newer versions, and if one is available, will guide you through the decisions you'd need to  
make.
```

```
## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("ppcor")#To check for correlations between independent variables
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine
```

```
library(lme4)
library(car)
library(ggplot2)
library(modEvA)
library(languageR)
library(ppcor)
library(AICcmodavg)
library(MuMIn)
library(dplyr)
library(sjPlot)
```

```
#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()
```

```
## Upload data
factors_original<-read.csv("factors_originalv1.csv")
```

```
##### Flip the variables for pb1-r1 so R1 is the focal group in all the encounters with decided outcome
```

```
#Checking the original data
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]
```

```
#Flipping pb1-r1 to r1-pb1
factors_original$winner_analysis[ factors_original$dyad=="pb1r1"] <-1-
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_groupsize[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_groupsize[
factors_original$dyad=="pb1r1"]
factors_original$rel_nummales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_nummales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numfemales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numfemales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numinfperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfperfem[
factors_original$dyad=="pb1r1"]
```

```
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfpermale[
factors_original$dyad=="pb1r1"]
factors_original$rel_numswfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numswfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swgs[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swgs[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfemperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfemperfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfempermale[
factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_sexratio[
factors_original$dyad=="pb1r1"]
factors_original$rel_UD190[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_UD190[factors_original$dyad=="pb1r1"]
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"]
```

#Checking that the flipping worked

```
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]
```

###Convert variables to the appropriate format

```
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$winner_analysis<- as.numeric(factors_original$winner_analysis)#If written as factor at this
stage, the flipping goes wrong
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$rel_numfemales<- as.numeric(factors_original$rel_numfemales)
factors_original$rel_nummales<- as.numeric(factors_original$rel_nummales)
factors_original$rel_numinfperfem<- as.numeric(factors_original$rel_numinfperfem)
factors_original$rel_numinfpermale<- as.numeric(factors_original$rel_numinfpermale)
factors_original$rel_numswfem<- as.numeric(factors_original$rel_numswfem)
factors_original$rel_swgs<- as.numeric(factors_original$rel_swgs)
factors_original$rel_swfemperfem<- as.numeric(factors_original$rel_swfemperfem)
factors_original$rel_swfempermale<- as.numeric(factors_original$rel_swfempermale)
factors_original$rel_sexratio<- as.numeric(factors_original$rel_sexratio)
factors_original$rel_UD190<- as.numeric(factors_original$rel_UD190)
factors_original$rel_distancetocorearea<- as.numeric(factors_original$rel_distancetocorearea)
factors_original$winner_analysis<- as.factor(factors_original$winner_analysis)#Now we can transform it into
factor without problems
```

#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison cannot be made)

```
missinggrows = is.na(factors_original$rel_nummales)
factors_original = factors_original[!missinggrows,]
missinggrows = is.na(factors_original$rel_numfemales)
factors_original= factors_original[!missinggrows,]
missinggrows = is.na(factors_original$rel_numinfperfem)
factors_original= factors_original[!missinggrows,]
missinggrows = is.na(factors_original$rel_numinfpermale)
factors_original= factors_original[!missinggrows,]
missinggrows = is.na(factors_original$rel_swfemperfem)
factors_original= factors_original[!missinggrows,]
```

```
missingrows = is.na(factors_original$rel_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_sexratio)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$winner_analysis)
factors_original= factors_original[!missingrows,]

cat("\n\n\n Checking correlations between fixed effects \n\n\n")

#Correlations between variables for the female-based models
fdata<-
data.frame(factors_original$rel_numfemales,factors_original$rel_numinfpermale,factors_original$rel_swfempermale,factors_original$rel_sexratio,factors_original$rel_UD190,factors_original$rel_distancetocorearea)
pcor(fdata)

#Correlations between variables for the male-based models
mdata<-
data.frame(factors_original$rel_nummales,factors_original$rel_numinfpermale,factors_original$rel_swfempermale,factors_original$rel_sexratio,factors_original$rel_UD190,factors_original$rel_distancetocorearea)
pcor(mdata)

cat("\n\n\n\n\n Checking potential control variables \n\n\n\n\n")
#null model

res.null=glmer(winner_analysis ~ 1+ (1|dyad), family="binomial", data=factors_original)

#AIC values to the list
models<-list()
models[[1]]<-res.null
Modnames <- "Empty null model"

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null<-r.squaredGLMM(res.null)
R2<-r2_null

cat("\n\n\n Checking potential control variables: Duration and number of observers \n\n\n")

res_cv=glmer(winner_analysis ~durationlGE+num_obs+(1|dyad), family="binomial", data=factors_original)

print(summary(res_cv))

#Comparison between the null model and the model with c.v
print(anova(res.null,res_cv, test="Chisq"))

#Check that no combination between response and random effects is too unfrequent
table(factors_original$winner_analysis, factors_original$dyad)
```

```
cat("\n\n\n\n\n\n\n Female-based model with use of space \n\n\n\n\n\n\n")

# Response: winner_analysis (binary,1=Focal group wins, 0= Focal group loses)
# Fixed effects: rel_numfemales+rel_numinfperfem+rel_swfemperferm+rel_sexratio+rel_UD190
# Random effect: 'dyad', 2 levels.
# Hypothesis: "A group would have increased odds of winning (1) when its number of females was larger than
its opponent,
# (2) when the proportion of infants/female is smaller (3) when the proportion of fertile females/female is
smaller
# (4) when the sex ratios (f:m) is higher than those of the opponent


#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(winner_analysis ~ rel_numfemales+rel_numinfperfem+rel_swfemperferm+rel_sexratio+rel_UD190,
family="binomial", data=factors_original))

#Run the model
res_fOud=glmer(winner_analysis ~
               rel_numfemales+rel_numinfperfem+rel_swfemperferm+rel_sexratio+rel_UD190+
               (1| dyad), family="binomial", data=factors_original)

print(summary(res_fOud))

cat("\n\n\n Comparison of female-based (full; UD) model to null model\n\n\n")

print(anova(res.null,res_fOud, test="Chisq"))

#AIC values to the list
models[[2]]<-res_fOud
Modnames <- rbind(Modnames, "Full Female based model (UD)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_fOud<-r.squaredGLMM(res_fOud)
R2<-rbind(R2,r2_fOud)

# All the variables except the number of infants are significant and retained


#Run the model
res_fud=glmer(winner_analysis ~
              rel_numfemales+rel_swfemperferm+rel_sexratio+rel_UD190+
              (1| dyad), family="binomial", data=factors_original)

print(summary(res_fud))

cat("\n\n\n Comparison of female-based (UD) model to null model\n\n\n")
print(anova(res.null,res_fud, test="Chisq"))

#AIC values to the list
models[[3]]<-res_fud
Modnames <- rbind(Modnames, "Female based model (UD)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_fud<-r.squaredGLMM(res_fud)
```



```
vif(glm(winner_analysis ~ rel_nummales+rel_numinfpermale+rel_swfempermale+rel_UD190,
family="binomial", data=factors_original))
vif(glm(winner_analysis ~ rel_nummales+rel_swfempermale+rel_sexratio+rel_UD190, family="binomial",
data=factors_original))
#Two separated sets of models will be done, excluding one of the problematic variables in each

cat("\n\n\n\n Male-based model 1 (no rel_sexratio) \n\n\n")
#Run full the model

res_mfull1=glmer(winner_analysis ~ rel_nummales+rel_numinfpermale+rel_swfempermale+rel_UD190+
(1|dyad), family="binomial", data=factors_original)

print(summary(res_mfull1))

cat("\n\n\n\n Comparison of male based model (full1) to null model\n\n\n")
print(anova(res.null,res_mfull1, test="Chisq"))
#The full model wasn't significant (but almost) so no adj. model is produced

#AIC values to the list
models[[5]]<-res_mfull1
Modnames <- rbind(Modnames, "Male based (i.u. full, minus sex ratio)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_mfull1<-r.squaredGLMM(res_mfull1)
R2<-rbind(R2,r2_mfull1)

plotLMER.fnc(res_ud,ylimit=0:1,lockYlim=TRUE,linecolor="dark green",
lwd=4,
ylabel="Probability of winning the encounter")


cat("\n\n\n\n\n Male-based model 2 (no rel_numinfpermale) \n\n\n\n")
#Run the model

res_mfull2=glmer(winner_analysis ~ rel_nummales+rel_swfempermale+rel_sexratio+rel_UD190+
(1|dyad), family="binomial", data=factors_original)

print(summary(res_mfull2))

cat("\n\n\n\n\n Comparison of male based model 2 (full) to null model\n\n\n\n")
print(anova(res.null,res_mfull2, test="Chisq"))

#AIC values to the list
models[[6]]<-res_mfull2
Modnames <- rbind(Modnames, "Male based (i.u. full, minus pr.infants)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_mfull2<-r.squaredGLMM(res_mfull2)
R2<-rbind(R2,r2_mfull2)

cat("\n\n\n\n\n\n\n\n\n\n\n Male-based model with core area \n\n\n\n\n\n\n\n\n\n\n")
```

```
# Response: winner_analysis (binary, 1=Focal group wins, 0= Focal group loses)
# Control variable/s: none
# Fixed effects: rel_nummales+rel_numinfpermale+rel_swfempermale+rel_sexratio+core_yn
# Random effect: 'dyad', 2 levels.
# Hypothesis: A group would have increased odds of winning (1) when it was larger than its opponent, (4) when
the proportion of infants/male is
# higher (5a) If mate defense by intergroup aggression, when the proportion of fertile females/male is higher,
the group would have more
# chances to win (5b) if mate defence by consortship, the lower the proportion of fertile females/male, the
higher the chances of winning
# (6) No effect on the sex ratio
```

```
#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(winner_analysis ~ rel_nummales+rel_numinfpermale+rel_swfempermale+rel_sexratio+core_yn,
family="binomial", data=factors_original))
```

```
# again problematic
vif(glm(winner_analysis ~ rel_nummales+rel_swfempermale+rel_sexratio+core_yn, family="binomial",
data=factors_original))
#Analyses will be separate in two
vif(glm(winner_analysis ~ rel_nummales+rel_numinfpermale+rel_swfempermale+core_yn, family="binomial",
data=factors_original))
```

```
cat("\n\n\n\n Male-based model (no sexratio) \n\n\n")
#Run the model
```

```
res_mfullc1=glmer(winner_analysis ~ rel_nummales+rel_numinfpermale+rel_swfempermale+core_yn+
(1|dyad), family="binomial", data=factors_original)
```

```
print(summary(res_mfullc1))
```

```
cat("\n\n\n\n Comparison of male based model (full) to null model\n\n\n")
print(anova(res.null, res_mfullc1, test="Chisq"))
```

```
#AIC values to the list
models[[7]]<-res_mfullc1
Modnames <- rbind(Modnames, "Male based (core, full minus s.ratio)")
```

```
#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_mfullc<-r.squaredGLMM(res_mfullc1)
R2<-rbind(R2, r2_mfullc)
```

```
cat("\n\n\n\n\n Male-based model (no infants) \n\n\n")
#Run the model
```

```
res_mfullc2=glmer(winner_analysis ~ rel_nummales+rel_swfempermale+rel_sexratio+core_yn+
(1|dyad), family="binomial", data=factors_original)
```

```

print(summary(res_mfullc2))

cat("\n\n Comparison of male based model (full2) to null model\n\n")
print(anova(res.null,res_mfullc2, test="Chisq"))

#AIC values to the list
models[[8]]<-res_mfullc2
Modnames <- rbind(Modnames, "Male based (core, full minus pr.infants)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_mfullc2<-r.squaredGLMM(res_mfullc2)
R2<-rbind(R2,r2_mfullc2)

#####
#####
#####
cat("\n\n RESULTS \n\n")
aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2

#Graphs of the best model
sjp.glmer(res_fud, type="pred", facet.grid=FALSE, vars="rel_numfemales",
  geom.colors = "bw",show.ci=TRUE)
sjp.glmer(res_fud, type="pred", facet.grid=FALSE, vars="rel_swfemperfem",
  geom.colors = "bw",show.ci=TRUE)
sjp.glmer(res_fud, type="pred", facet.grid=FALSE, vars="rel_sexratio",
  geom.colors = "bw",show.ci=TRUE)
sjp.glmer(res_fud, type="pred", facet.grid=FALSE, vars="rel_UD190",
  geom.colors = "bw",show.ci=TRUE)

cat("\n\n Comparison with the best model of the previous chapter \n\n")

res_gsud=glmer(winner_analysis ~ rel_groupsize+rel_UD190+rel_groupsize*rel_UD190+
  (1|dyad), family="binomial", data=factors_original)

print(summary(res_gsud))

cat("\n\n Comparison of group size+IU based model to null model\n\n")
print(anova(res.null,res_gsud, test="Chisq"))

#AIC values to the list
models[[9]]<-res_gsud
Modnames <- rbind(Modnames, "Group size+I.U")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_gsud<-r.squaredGLMM(res_gsud)
R2<-rbind(R2,res_gsud)

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2

```



```
factors_original$abs_numfemales<- as.numeric(factors_original$abs_numfemales)
factors_original$abs_nummales<- as.numeric(factors_original$abs_nummales)
factors_original$abs_numinfperfem<- as.numeric(factors_original$abs_numinfperfem)
factors_original$abs_numinfpermale<- as.numeric(factors_original$abs_numinfpermale)
factors_original$abs_swfemperfem<- as.numeric(factors_original$abs_swfemperfem)
factors_original$abs_swfempermale<- as.numeric(factors_original$abs_swfempermale)
factors_original$abs_sexratio<- as.numeric(factors_original$abs_sexratio)
factors_original$core_yn <- factor(factors_original$core_yn)
factors_original$abs_UD190<- as.numeric(factors_original$abs_UD190)
factors_original$abs_distancetocorearea<- as.numeric(factors_original$abs_distancetocorearea)
```

#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison cannot be made)

```
missingrows = is.na(factors_original$ abs_nummales)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numfemales)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numinfperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numinfpermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_swfemperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_sexratio)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$aggression_yn)
factors_original= factors_original[!missingrows,]
```

```
table(factors_original$aggression_yn, factors_original$dyad)
```

```
cat("\n\n\n\n\n\n\n Checking potential control variables \n\n\n\n\n\n\n")
```

```
#Empty null model
```

```
resa.null0=glmer(aggression_yn ~ 1+ (1|dyad), family="binomial", data=factors_original)
```

```
#AIC values to the list
```

```
models<-list()
```

```
models[[1]]<-resa.null0
```

```
Modnames <- "Empty null model"
```

```
#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
```

```
r2_null0<-r.squaredGLMM(resa.null0)
```

```
R2_a<-r2_null0
```

```
cat("\n\n\n\n\n\n\n Checking potential control variables: Duration and number of observers \n\n\n")
```

```
resa_cv=glmer(aggression_yn ~ durationlGE+num_obs+(1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resa_cv))
```

```

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resa.null0,resa_cv, test="Chisq"))

#Only duration significant

resa.null=glmer(aggression_yn ~ durationIGE+(1|dyad), family="binomial", data=factors_original)

print(summary(resa.null))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resa.null0,resa.null, test="Chisq"))

#Duration will be control variable

#AIC values to the list
models[[2]]<-resa.null
Modnames <- rbind(Modnames,"Null model (c.v)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null<-r.squaredGLMM(resa.null)
R2_a<-rbind(R2_a,r2_null)

plotLMER.fnc(resa.null,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of Aggressive Encounter")

cat("\n\n\n Female-based model \n\n\n")

cat("\n\n\n Intensity of Use of space \n\n\n")
# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables: num_obs and durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_yn ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=factors_original))

#Run the model
resa_fud=glmer(aggression_yn ~
              abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190+durationIGE+
              (1|dyad), family="binomial", data=factors_original)

print(summary(resa_fud))

cat ("\n\n\n Comparison of female-based model (full) to null model\n\n\n")

print(anova(resa.null,resa_fud, test="Chisq"))

```

```
#AIC values to the list
models[[3]]<-resa_fud
Modnames <- rbind(Modnames,"Full female model (i.u)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_fud<-r.squaredGLMM(resa_fud)
R2_a<-rbind(R2_a,r2_fud)

cat("\n\n Distance to core area\n\n")
# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables: num_obs and durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_yn ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea+durationIGE,
family="binomial", data=factors_original))

#Run the model
resa_fdc=glmer(aggression_yn ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea+durationIGE+
(1|dyad), family="binomial", data=factors_original)

print(summary(resa_fdc))

cat ("\n\n Comparison of female-based model (full, dc) to null model\n\n")

print(anova(resa.null,resa_fdc, test="Chisq"))

#AIC values to the list
models[[4]]<-resa_fdc
Modnames <- rbind(Modnames,"Full female model (d.c.)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_fdc<-r.squaredGLMM(resa_fdc)
R2_a<-rbind(R2_a,r2_fdc)

cat("\n\n Categorical d.core\n\n")
# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables: num_obs and durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
```

#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the proportion of infants/female
 # is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)

```
vif(glm(aggression_yn ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+durationIGE+core_yn,
family="binomial", data=factors_original))
```

#Run the model

```
resa_fc=glmer(aggression_yn ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn+durationIGE+
(1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resa_fc))
```

```
cat("\n\n Comparison of female-based model (full) to null model\n\n")
```

```
print(anova(resa.null,resa_fc, test="Chisq"))
```

#AIC values to the list

```
models[[5]]<-resa_fc
```

```
Modnames <- rbind(Modnames,"Full female model (c.c.)")
```

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)

```
r2_fc<-r.squaredGLMM(resa_fc)
```

```
R2_a<-rbind(R2_a,r2_fc)
```

```
cat("\n\n Male-based model\n\n")
```

```
cat("\n\n Intensity of use \n\n")
```

Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)

Control variables: num_obs and durationIGE

Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn

Random effect: 'dyad', 3 levels.

Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the proportion of infants/male is higher (3)

when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)

```
vif(glm(aggression_yn ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=factors_original))
```

```
vif(glm(aggression_yn ~ abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190+durationIGE,
family="binomial", data=factors_original))
```

```
vif(glm(aggression_yn ~ +abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=factors_original))
```

#Run the model (full male i.u. no sex ratio)

```

resa_mud1=glmer(aggression_yn ~
  abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resa_mud1))

cat("\n\n Comparison of male-based model 1 (full no sex ratio) to null model\n\n")
print(anova(resa.null,resa_mud1, test="Chisq"))

#AIC values to the list
models[[6]]<-resa_mud1
Modnames <- rbind(Modnames,"Full male model (i.u, no sex ratio)")

#Calculating Marginal and Conditional R2
r2_mud1<-r.squaredGLMM(resa_mud1)
R2_a<-rbind(R2_a,r2_mud1)

#Run the model (full male i.u. no abs_nummales)
resa_mud2=glmer(aggression_yn ~
  abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resa_mud2))

cat("\n\n Comparison of male-based model 1 (full no sex ratio) to null model\n\n")
print(anova(resa.null,resa_mud2, test="Chisq"))

#AIC values to the list
models[[7]]<-resa_mud2
Modnames <- rbind(Modnames,"Full male model (i.u, no No.males)")

#Calculating Marginal and Conditional R2
r2_mud2<-r.squaredGLMM(resa_mud2)
R2_a<-rbind(R2_a,r2_mud2)

cat("\n\n Distance to core\n\n")
# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables: num_obs and durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the
proportion of infants/male is higher (3)
# when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)

```

```

vif(glm(aggression_yn ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE,
family="binomial", data=factors_original))

vif(glm(aggression_yn ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea+durationIGE,
family="binomial", data=factors_original))
vif(glm(aggression_yn ~
abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE,
family="binomial", data=factors_original))

#Run the model Male-based model (no ser ratio)
resa_mdc1=glmer(aggression_yn ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea++durationIGE+
(1|dyad), family="binomial", data=factors_original)

print(summary(resa_mdc1))

cat("\n\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resa.null,resa_mdc1, test="Chisq"))

#Only duration was significant
#AIC values to the list
models[[8]]<-resa_mdc1
Modnames <- rbind(Modnames,"Full male model (d.c., no sex ratio)")

#Calculating Marginal and Conditional R2
r2_mdc1<-r.squaredGLMM(resa_mdc1)
R2_a<-rbind(R2_a,r2_mdc1)

#Run the model Male-based model (no No.males)
resa_mdc2=glmer(aggression_yn ~
abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea++durationIGE+
(1|dyad), family="binomial", data=factors_original)

print(summary(resa_mdc2))

cat("\n\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resa.null,resa_mdc2, test="Chisq"))

#Only duration was significant
#AIC values to the list
models[[9]]<-resa_mdc2
Modnames <- rbind(Modnames,"Full male model (d.c., no No.males)")

#Calculating Marginal and Conditional R2
r2_mdc2<-r.squaredGLMM(resa_mdc2)
R2_a<-rbind(R2_a,r2_mdc2)

cat("\n\n\n Categorical d.core\n\n")
# Response: aggression_yn (binary,1=Aggressive IGE, 0=Non-aggressive IGE)
# Control variables: num_obs and durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.

```

Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the proportion of infants/male is higher (3)
 # when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
 vif(glm(aggression_yn ~
 abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn+durationIGE,
 family="binomial", data=factors_original))
 #Although the vif of sex ratio is >2, is <3, so no action taken

#Run the model
 resa_mcc=glmer(aggression_yn ~
 abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn+durationIGE+
 (1|dyad), family="binomial", data=factors_original)

print(summary(resa_mcc))

cat("\n\n\n Comparison of male-based model 1 (full) to null model\n\n")
 print(anova(resa.null,resa_mcc, test="Chisq"))

#AIC values to the list
 models[[10]]<-resa_mcc
 Modnames <- rbind(Modnames,"Full male model (c.c.)")

#Calculating Marginal and Conditional R2
 r2_mcc<-r.squaredGLMM(resa_mcc)
 R2_a<-rbind(R2_a,r2_mcc)

cat("\n\n\n SUMMARY RESULTS \n\n\n")
 aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nob = NULL, sort = TRUE)
 R2_a

aictab<-aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nob = NULL, sort = TRUE)
 evidence(aictab, model.high = "top", model.low = "second.ranked")
 evidence(aictab, model.high = "top", model.low = "Full male model (d.c., no sex ratio)")
 evidence(aictab, model.high = "top", model.low = "Full male model (d.c., no No.males)")
 evidence(aictab, model.high = "top", model.low = "Full male model (c.c.)")
 evidence(aictab, model.high = "top", model.low = "Full male model (i.u, no No.males)")
 evidence(aictab, model.high = "top", model.low = "Full female model (d.c.)")
 evidence(aictab, model.high = "top", model.low = "Full female model (i.u)")
 evidence(aictab, model.high = "top", model.low = "Full female model (c.c.)")
 evidence(aictab, model.high = "top", model.low = "Empty null model")

3.1.5. MODELS PREDICTING THE PROBABILITY OF FEMALE AND MALE AGGRESSION AND HERDING.

```
## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr

# using the package:
updateR() # this will start the updating process of your R installation. It will check for newer versions, and if one
is available, will guide you through the decisions you'd need to make.

## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("ppcor")#To check for correlations between independent variables
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine

library(lme4)
library(car)
library(ggplot2)
library(modEvA)
library(languageR)
library(ppcor)
library(AICcmodavg)
library(MuMIn)
library(dplyr)
library(sjPlot)

#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()

#####
#####
cat("\n\n\n\n\n\n\n Female and male aggression during IGE\n\n\n\n\n\n\n")
#####
#####

cat("\n\n\n\n\n\n\n FACTORS AFFECTING FEMALE AGGRESSION\n\n\n\n\n\n\n")

## Upload data
```

```
factors_original<-read.csv("factors_originalv1.csv")
####Convert variables to the appropriate format
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$aggression_yn <- factor(factors_original$aggression_yn)
factors_original$aggression_m <- factor(factors_original$aggression_m)
factors_original$aggression_f <- factor(factors_original$aggression_f)
factors_original$wg_herding <- factor(factors_original$wg_herding)
factors_original$abs_numfemales<- as.numeric(factors_original$abs_numfemales)
factors_original$abs_nummales<- as.numeric(factors_original$abs_nummales)
factors_original$abs_numinfperfem<- as.numeric(factors_original$abs_numinfperfem)
factors_original$abs_numinfpermale<- as.numeric(factors_original$abs_numinfpermale)
factors_original$abs_swfemperfem<- as.numeric(factors_original$abs_swfemperfem)
factors_original$abs_swfempermale<- as.numeric(factors_original$abs_swfempermale)
factors_original$abs_sexratio<- as.numeric(factors_original$abs_sexratio)
factors_original$sum_sexratios<- as.numeric(factors_original$sum_sexratios)
factors_original$sum_swfempermale<- as.numeric(factors_original$sum_swfempermale)
factors_original$core_yn <- factor(factors_original$core_yn)
factors_original$abs_UD190<- as.numeric(factors_original$abs_UD190)
factors_original$abs_distancetocorearea<- as.numeric(factors_original$abs_distancetocorearea)
```

#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison cannot be made)

```
missingrows = is.na(factors_original$ abs_nummales)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numfemales)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numinfperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$sum_sexratios)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$sum_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$aggression_f)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$aggression_m)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$wg_herding)
factors_original= factors_original[!missingrows,]
```

```
ag_dyad<-table(factors_original$aggression_yn, factors_original$dyad)
chisq.test(ag_dyad)
```

```
fag_dyad<-table(factors_original$aggression_f, factors_original$dyad)
chisq.test(fag_dyad)
```

```
mag_dyad<-table(factors_original$aggression_m, factors_original$dyad)
chisq.test(mag_dyad)
```

```
fag_cag<-table(factors_original$aggression_f, factors_original$contact_aggresion)
chisq.test(fag_cag)
```

```
mag_cag<-table(factors_original$aggression_m, factors_original$contact_aggresion)
chisq.test(mag_cag)
```

```
##The null model

resaf.null0=glmer(aggression_f ~ 1+ (1|dyad), family="binomial", data=factors_original)

#AIC values to the list
modelsf<-list()
modelsf[[1]]<-resaf.null0
Modnamesf <- "Empty null model"

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null0<-r.squaredGLMM(resaf.null0)
R2_f<-r2_null0

cat("\n\n\ Checking potential control variables: Duration and number of observers \n\n")

resaf.null=glmer(aggression_f ~ durationIGE+num_obs+sum_f+(1|dyad), family="binomial",
data=factors_original)

print(summary(resaf.null))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resaf.null0,resaf.null, test="Chisq"))

#Both, duration and number of observers influenced whether female aggression was observed

#AIC values to the list
modelsf[[2]]<-resaf.null
Modnamesf <- rbind(Modnamesf,"Null model (c.v) ")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null<-r.squaredGLMM(resaf.null)
R2_f<-rbind(R2_f,r2_null)

plotLMER.fnc(resaf.null,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of female aggression")

cat("\n\n\n\n SOCIO-ECOLOGICAL MODEL (no male strategies considered) \n\n\n\n")
# According to the socioecological models, females would be particularly willing to fight against other groups
when interesting
# resources are on stake. The number of fertile females shouldn't matter, but the number of infants should
increase aggression
# (maybe not from the mothers if the babies are still dependent, but at least from the matriline). This would
ignore any male
# related variable, as the socioecological models do. Thus, female aggression would be more likely to happen: 1)
the more similar the groups were
```


in number of females; 2) the most used is the area where the IGE happens (measured independently with the 3 location-based-payoffs), and
 # 3) The more similar they were in number of infants.

```
cat("\n\n I.U. \n\n")
#vif
vif(glm(aggression_f ~ abs_numfemales+abs_numinfperfem+abs_UD190+durationIGE+num_obs+sum_f,
family="binomial", data=factors_original))

resaf_seiu=glmer(aggression_f ~
abs_numfemales+abs_numinfperfem+abs_UD190+durationIGE+num_obs+sum_f+(1|dyad), family="binomial",
data=factors_original)

print(summary(resaf_seiu))
# Only the control variable duration was significant

#Comparison between the null model and the full socioecological model
print(anova(resaf.null,resaf_seiu, test="Chisq"))
#Not significantly different from the null model (actually, it's worse)

#AIC values to the list
modelsf[[3]]<-resaf_seiu
Modnamesf <- rbind(Modnamesf,"Socioecological model (i.u)")

#Calculating Marginal and Conditional R2
r2_seiu<-r.squaredGLMM(resaf_seiu)
R2_f<-rbind(R2_f,r2_seiu)

plotLMER.fnc(resaf_seiu,ylim=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,xlabel="Duration IGE",
ylabel="Probability of female aggression ")

cat("\n\n Distance to core \n\n")

#vif
vif(glm(aggression_f ~
abs_numfemales+abs_numinfperfem+abs_distancetocorearea+durationIGE+num_obs+sum_f,
family="binomial", data=factors_original))

resaf_sedc=glmer(aggression_f ~
abs_numfemales+abs_numinfperfem+abs_distancetocorearea+durationIGE+num_obs+sum_f+(1|dyad),
family="binomial", data=factors_original)

print(summary(resaf_sedc))

#Comparison between the null model and the full socioecological model
print(anova(resaf.null,resaf_sedc, test="Chisq"))
```

```
#Not significantly different from the null model (actually, it's worse)

#AIC values to the list
modelsf[[4]]<-resaf_sedc
Modnamesf <- rbind(Modnamesf,"Socioecological model (d.c.)")

#Calculating Marginal and Conditional R2
r2_sedc<-r.squaredGLMM(resaf_sedc)
R2_f<-rbind(R2_f,r2_sedc)

plotLMER.fnc(resaf_sedc,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of female aggression ")

cat("\n\n\ Categorical core area \n\n")

#vif
vif(glm(aggression_f ~ abs_numfemales+abs_numinfperfm+core_yn+durationIGE+num_obs+sum_f,
family="binomial", data=factors_original))

resaf_secc=glmer(aggression_f ~
abs_numfemales+abs_numinfperfm+core_yn+durationIGE+num_obs+sum_f+(1|dyad), family="binomial",
data=factors_original)

print(summary(resaf_secc))

#Comparison between the null model and the full socioecological model (c.c.)
print(anova(resaf.null,resaf_secc, test="Chisq"))
#Not significantly different from the null model (actually, it's worse)

#AIC values to the list
modelsf[[5]]<-resaf_secc
Modnamesf <- rbind(Modnamesf,"Socioecological model (c.c.)")

#Calculating Marginal and Conditional R2
r2_secc<-r.squaredGLMM(resaf_secc)
R2_f<-rbind(R2_f,r2_secc)

plotLMER.fnc(resaf_secc,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of female aggression ")

cat("\n\n\n\n\ MALE HERDING CONSIDERED\n\n\n\n")
# Male interest however may hinder female participation by herding and consortship.
# If so, sex ratio, proportion of fertile females per male, and male aggression might be more explanatory than
# the typical factors considered.
```

```
# Thus, female aggression will be more likely 1) The greater the sum of sex ratios (the more females per male
# in total, the more likely some are able to aggress); 2) The smaller the sum of fertile females per male (less
# likely to
# be driven away when they are not fertile)3) When there is there is male aggression ( so females can join while
# the males are busy
# without being attack themselves); 4) when there is no herding recorded
```

```
#vif
vif(glm(aggression_f ~
sum_sexratios+sum_swfempermale+aggression_m+wg_herding+durationIGE+num_obs+sum_f,
family="binomial", data=factors_original))
```

```
resaf_ms=glmer(aggression_f ~
sum_sexratios+sum_swfempermale+aggression_m+wg_herding+durationIGE+num_obs+sum_f+(1|dyad),
family="binomial", data=factors_original)
```

```
print(summary(resaf_ms))
```

```
#Comparison between the null model and the full male strategies
print(anova(resaf.null,resaf_ms, test="Chisq"))
```

```
#An adjusted model will be performed with the control variables and male aggression (only significant variables)
```

```
#AIC values to the list
modelsf[[6]]<-resaf_ms
Modnamesf <- rbind(Modnamesf,"Full male strategies model")
```

```
#Calculating Marginal and Conditional R2
r2_ms<-r.squaredGLMM(resaf_ms)
R2_f<-rbind(R2_f,r2_ms)
```

```
plotLMER.fnc(resaf_ms,ylimit=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,xlabel="Duration IGE",
ylabel="Probability of female aggression ")
```

```
##Adjusted male-strategies model
```

```
resaf_ms2=glmer(aggression_f ~ aggression_m+durationIGE+num_obs+sum_f+(1|dyad), family="binomial",
data=factors_original)
```

```
print(summary(resaf_ms2))
```

```
#Comparison between the null model and the full male strategies
print(anova(resaf.null,resaf_ms2, test="Chisq"))
```

```
#AIC values to the list
modelsf[[7]]<-resaf_ms2
```

```

Modnamesf <- rbind(Modnamesf,"Adj. male strategies model")

#Calculating Marginal and Conditional R2
r2_ms2<-r.squaredGLMM(resaf_ms2)
R2_f<-rbind(R2_f,r2_ms2)

plotLMER.fnc(resaf_ms2,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of female aggression ")

cat("\n\n\n\n Females as male supporters \n\n\n\n")

resaf_sup=glmer(aggression_f ~
aggression_m+abs_UD190+abs_nummales+durationIGE+num_obs+sum_f+(1|dyad), family="binomial",
data=factors_original)

print(summary(resaf_sup))

#AIC values to the list
modelsf[[8]]<-resaf_sup
Modnamesf <- rbind(Modnamesf,"Supporters")

#Calculating Marginal and Conditional R2
r2_sup<-r.squaredGLMM(resaf_sup)
R2_f<-rbind(R2_f,r2_sup)

sjp.glmer(resaf_sup, type="pred", facet.grid=FALSE, vars="abs_nummales",
          geom.colors = "bw",show.ci=TRUE)

####SUMMARY OF RESULTS####

aictab(cand.set=modelsf, modnames = Modnamesf, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_f

aictabf<-aictab(cand.set=modelsf, modnames = Modnamesf, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictabf, model.high = "top", model.low = "second.ranked")
evidence(aictabf, model.high = "top", model.low = "Full male strategies model")
evidence(aictabf, model.high = "top", model.low = "male strategies model (sum_m)")
evidence(aictabf, model.high = "top", model.low = "Null model (c.v) ")
evidence(aictabf, model.high = "top", model.low = "Socioecological model (i.u)")
evidence(aictabf, model.high = "top", model.low = "Socioecological model (d.c.)")
evidence(aictabf, model.high = "top", model.low = "Socioecological model (c.c.)")
evidence(aictabf, model.high = "top", model.low = "Empty null model")

sjp.glmer(resaf_ms2, type="pred", facet.grid=FALSE, vars="durationIGE",
          geom.colors = "bw",show.ci=TRUE)
sjp.glmer(resaf_ms2, type="pred", facet.grid=FALSE, vars="num_obs",

```

```

models<-list()
models[[1]]<-resam.null0
Modnamesm <- "Empty null model"

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null0<-r.squaredGLMM(resam.null0)
R2_m<-r2_null0

cat("\n\n Checking potential control variables: Duration, number of observers and total number of males \n\n")

resam_cv=glmer(aggression_m ~ durationIGE+num_obs+sum_m+(1|dyad), family="binomial",
data=factors_original)

print(summary(resam_cv))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resam.null0,resam_cv, test="Chisq"))

resam.null=glmer(aggression_m ~ durationIGE+(1|dyad), family="binomial", data=factors_original)

print(summary(resam.null))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resam.null0,resam.null, test="Chisq"))

#AIC values to the list
models[[2]]<-resam.null
Modnamesm <- rbind(Modnamesm,"Null model (c.v) ")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null<-r.squaredGLMM(resam.null)
R2_m<-rbind(R2_m,r2_null)

plotLMER.fnc(resam.null,ylimit=0:1,lockYlim=TRUE,linecolor="red",
lwd=4,xlabel="Duration IGE",
ylabel="Probability of male aggression")

cat("\n\n\n\n MALE MATE DEFENSE\n\n\n\n")
# Males may defend access to females during intergroup encounters; either by attacking the other group (hired
guns)
# of by attacking the females of their own group (see Fashing 2001)

cat("\n\n\n Hired guns\n\n")
# Males would aggress the other group more frequently when there are more fertile females, the other group is
similar in number
# of males and females are aggressive

resam_hg=glmer(aggression_m ~ sum_swfempermale+abs_nummales+aggression_f+durationIGE+(1|dyad),
family="binomial", data=factors_original)

print(summary(resam_hg))

```

```
#Comparison between the null model and the model for hired guns
print(anova(resam.null,resam_hg, test="Chisq"))

#AIC values to the list
modelsm[[3]]<-resam_hg
Modnamesm <- rbind(Modnamesm,"Full hired guns")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_hg<-r.squaredGLMM(resam_hg)
R2_m<-rbind(R2_m,r2_hg)

plotLMER.fnc(resam_hg,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of male aggression")

#Adjusted hired guns (only female partic)

resam_hg2=glmer(aggression_m ~ aggression_f+durationIGE+(1|dyad), family="binomial",
data=factors_original)

print(summary(resam_hg2))

#Comparison between the null model and the model for hired guns (adj)
print(anova(resam.null,resam_hg2, test="Chisq"))

#AIC values to the list
modelsm[[4]]<-resam_hg2
Modnamesm <- rbind(Modnamesm,"Adj. hired guns")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_hg2<-r.squaredGLMM(resam_hg2)
R2_m<-rbind(R2_m,r2_hg2)

plotLMER.fnc(resam_hg2,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of male aggression")

cat("\n\n Herders & consorters \n\n")
# If males protect access to females by aggressing the females themselves, male aggression towards the other
group would decrease
# with the proportion of fertile females, total proportion of females to males and with herding

resam_hd=glmer(aggression_m ~ sum_swfempermale+wg_herding+sum_sexratios+durationIGE+(1|dyad),
family="binomial", data=factors_original)

print(summary(resam_hd))

#Comparison between the null model and the model for hired guns
print(anova(resam.null,resam_hd, test="Chisq"))
```

```
#AIC values to the list
modelsm[[5]]<-resam_hd
Modnamesm <- rbind(Modnamesm,"Full herders model")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_hd<-r.squaredGLMM(resam_hd)
R2_m<-rbind(R2_m,r2_hd)

plotLMER.fnc(resam_hd,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of male aggression")

cat("\n\n\n\n MALE RESOURCE DEFENSE\n\n\n\n")

#Males may protect resources for females if these then prefer to mate with those who participate. Then the
agggression would depend on how much loction-based
# payoffs there is (i.e. when similar in value to other group, more aggression)

#Intensity of use
resam_iu=glmer(aggression_m ~abs_nummales+abs_UD190+durationIGE+(1|dyad), family="binomial",
data=factors_original)

print(summary(resam_iu))

#Comparison between the null model and the model for r.defense
print(anova(resam.null,resam_iu, test="Chisq"))

#AIC values to the list
modelsm[[6]]<-resam_iu
Modnamesm <- rbind(Modnamesm,"Resource defense (i.u)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_iu<-r.squaredGLMM(resam_iu)
R2_m<-rbind(R2_m,r2_iu)

plotLMER.fnc(resam_iu,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of male aggression")

#Distance to core
resam_dc=glmer(aggression_m ~abs_nummales+abs_distancetocorearea +durationIGE+(1|dyad),
family="binomial", data=factors_original)

print(summary(resam_dc))

#Comparison between the null model and the model for r.defense
print(anova(resam.null,resam_dc, test="Chisq"))
```



```

#AIC values to the list
modelsm[[7]]<-resam_dc
Modnamesm <- rbind(Modnamesm,"Resource defense (d.c)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_dc<-r.squaredGLMM(resam_dc)
R2_m<-rbind(R2_m,r2_dc)

plotLMER.fnc(resam_dc,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of male aggression")

#Categorical core
resam_cc=glmer(aggression_m ~abs_nummales+core_yn+durationIGE+(1|dyad), family="binomial",
data=factors_original)

print(summary(resam_cc))

#Comparison between the null model and the model for r.defense
print(anova(resam.null,resam_cc, test="Chisq"))

#AIC values to the list
modelsm[[8]]<-resam_cc
Modnamesm <- rbind(Modnamesm,"Resource defense (c.c)")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_cc<-r.squaredGLMM(resam_cc)
R2_m<-rbind(R2_m,r2_cc)

plotLMER.fnc(resam_cc,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of male aggression")

####SUMMARY OF RESULTS####

aictab(cand.set=modelsm, modnames = Modnamesm, second.ord = TRUE, nob = NULL, sort = TRUE)
R2_m

aictabm<-aictab(cand.set=modelsm, modnames = Modnamesm, second.ord = TRUE, nob = NULL, sort = TRUE)
evidence(aictabm, model.high = "top", model.low = "second.ranked")
evidence(aictabm, model.high = "top", model.low = "Null model (c.v) ")
evidence(aictabm, model.high = "top", model.low = "Resource defense (c.c)")
evidence(aictabm, model.high = "top", model.low = "Resource defense (d.c)")
evidence(aictabm, model.high = "top", model.low = "Resource defense (i.u)")
evidence(aictabm, model.high = "top", model.low = "Full herders model")
evidence(aictabm, model.high = "top", model.low = "Empty null model")

sjp.glmer(resam_hg, type="pred", facet.grid=FALSE, vars="durationIGE",
          geom.colors = "bw",show.ci=TRUE)
sjp.glmer(resam_hg, type="pred", facet.grid=FALSE, vars="aggression_f",
          geom.colors = "bw",show.ci=TRUE)

```

```

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null0<-r.squaredGLMM(resh.null0)
R2_h<-r2_null0

cat("\n\n\ Checking potential control variables: Duration and number of observers \n\n")

resh_cv=glmer(wg_herding ~ durationIGE+num_obs+(1|dyad), family="binomial", data=factors_original)

print(summary(resh_cv))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resh.null0,resh_cv, test="Chisq"))

#Only duration significant
resh.null=glmer(wg_herding ~ durationIGE+(1|dyad), family="binomial", data=factors_original)

print(summary(resh.null))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resh.null0,resh.null, test="Chisq"))

#AIC values to the list
modelsh[[2]]<-resh.null
Modnamesh <- rbind(Modnamesh,"Null model (c.v) ")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null<-r.squaredGLMM(resh.null)
R2_h<-rbind(R2_h,r2_null)

plotLMER.fnc(resh.null,ylim=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of herding")

cat("\n\n\n\n\ Herding as a male monopolization strategy of fertile females\n\n\n\n")
# Males would herd females more often 1)the smaller is the sex ratio (less female per male
# would imply that they are "more valuable" and that males would have better chances of herding with success),
# 2) When there are more fertile females (which are the ones thought to be most likely to be herded) and
# 3)when the difference
# between number of males is bigger (the males of the smaller group may put more effort in herding females as
# a better strategy
# to avoid them from mating with the numerous males of the other group)
vif(glm(wg_herding ~ sum_swfempermale+abs_nummales+sum_sexratios+durationIGE, family="binomial",
data=factors_original))

resh=glmer(wg_herding ~ sum_swfempermale+abs_nummales+sum_sexratios+durationIGE+(1|dyad),
family="binomial", data=factors_original)

print(summary(resh))

#Comparison between the null model and the model for hired guns
print(anova(resh.null,resh, test="Chisq"))

```

```
#AIC values to the list
modelsh[[3]]<-resh
Modnamesh <- rbind(Modnamesh,"Herding model")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_h<-r.squaredGLMM(resh)
R2_h<-rbind(R2_h,r2_h)

plotLMER.fnc(resh,ylimit=0:1,lockYlim=TRUE,linecolor="red",
             lwd=4,xlabel="Duration IGE",
             ylabel="Probability of herding")

#Summary of results
aictab(cand.set=modelsh, modnames = Modnamesh, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_h

aictabh<-aictab(cand.set=modelsh, modnames = Modnamesh, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictabh, model.high = "top", model.low = "second.ranked")
evidence(aictabh, model.high = "top", model.low = "Empty null model")

sjp.glmer(resh.null, type="pred", facet.grid=FALSE, vars="durationIGE",
          geom.colors = "bw",show.ci=TRUE,point.color=factors_original$cat_aggression)

##When doesn;t herding happen?

str(factors_original)

#Herding and aggression
ggplot(factors_original, aes(x=wg_herding))+
  geom_bar()+
  facet_wrap(~aggression_yn)

#Herding and contact aggression
ggplot(factors_original, aes(x=wg_herding))+
  geom_bar()+
  facet_wrap(~aggression_level)

#Herding and IG mating
ggplot(factors_original, aes(x=wg_herding))+
  geom_bar()+
  facet_wrap(~ig_mating)

tbl<-table(factors_original$wg_herding, factors_original$ig_mating,useNA="no")
tbl
chisq.test(tbl)

#Herding and IG female affiliation
ggplot(factors_original, aes(x=wg_herding))+
  geom_bar()+
  facet_wrap(~affiliation_f)

table(factors_original$wg_herding, factors_original$affiliation_f,useNA="no")

tbl<-table(factors_original$wg_herding, factors_original$affiliation_f,useNA="no")
```

```
chisq.test(tbl)

#Does it influence the changes of herding then?
missingrows = is.na(factors_original$affiliation_f)
factors_original= factors_original[!missingrows,]

reshf=glmer(wg_herding ~ affiliation_f+durationIGE+(1|dyad), family="binomial", data=factors_original)

print(summary(reshf))
reshf.null=glmer(wg_herding ~ durationIGE+(1|dyad), family="binomial", data=factors_original)

#Comparison between the null model
print(anova(reshf.null,reshf, test="Chisq"))

ggplot(factors_original, aes(x=affiliation_f,y=durationIGE))+
  geom_boxplot()

a=glmer(affiliation_f ~durationIGE+(1|dyad), family="binomial", data=factors_original)
print(summary(a))
r.squaredGLMM(a)

ggplot(factors_original, aes(x=wg_herding,y=sum_sexratios))+
  geom_boxplot()

ggplot(factors_original, aes(x=wg_herding,y=sum_swfempermale ))+
  geom_boxplot()
```

3.1.4. MODELS PREDICTING THE PROBABILITY OF PRESENCE OF CONTACT AGGRESSION IN AGGRESSIVE ENCOUNTERS

```
## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr

# using the package:
updateR() # this will start the updating process of your R installation. It will check for newer versions, and if one
is available, will guide you through the decisions you'd need to make.

## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("ppcor")#To check for correlations between independent variables
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
```



```
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$aggression_level)
factors_original= factors_original[!missingrows,]

table(factors_original$aggression_level, factors_original$dyad)

cat("\n\n\n\n\n Checking potential control variables \n\n\n\n\n")
#Empty null model

resal.null0=glmer(aggression_level ~ 1+ (1|dyad), family="binomial", data=factors_original)

#AIC values to the list
models<-list()
models[[1]]<-resal.null0
Modnames <- "Empty null model"

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null0<-r.squaredGLMM(resal.null0)
R2_al<-r2_null0

cat("\n\n\n Checking potential control variables: Duration and number of observers \n\n\n")

resal_cv=glmer(aggression_level ~ durationI GE+num_obs+(1|dyad), family="binomial", data=factors_original)

print(summary(resal_cv))

#Comparison between the null model and the model with potential control variables
print(anova(resal.null0,resal_cv, test="Chisq"))
#Duration was significant and too was the full model; duration will be used as control variable

resal.null=glmer(aggression_level ~ durationI GE+(1|dyad), family="binomial", data=factors_original)

print(summary(resal.null))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resal.null0,resal.null, test="Chisq"))

#AIC values to the list
models[[2]]<-resal.null
Modnames <- rbind(Modnames, "Null model")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null<-r.squaredGLMM(resal.null)
R2_al<-rbind(R2_al,r2_null)

cat("\n\n\n\n\n Female-based models \n\n\n\n\n")
```

```
cat("\n\n Intensity of use of space \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar
```

```
#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=factors_original))
```

```
#Run the model
resal_fud=glmer(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190+durationIGE+
(1|dyad), family="binomial", data=factors_original)
```

```
print(summary(resal_fud))
```

```
cat ("\n\n\n Comparison of female-based model (full, iu) to null model\n\n")
```

```
print(anova(resal.null,resal_fud, test="Chisq"))
```

```
#AIC values to the list
models[[3]]<-resal_fud
Modnames <- rbind(Modnames,"Female-based full model (i.u.)")
```

```
#Calculating Marginal and Conditional R2
r2_fud<-r.squaredGLMM(resal_fud)
R2_al<-rbind(R2_al,r2_fud)
```

```
cat("\n\n Distance to core area \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distance to core
area
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar
```

```
#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea+durationIGE,
family="binomial", data=factors_original))
```

```
#Run the model
resal_fdc=glmer(aggression_level ~
```



```
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resal_fdc))

cat("\n\n\n Comparison of female-based model (full, dc) to null model\n\n")

print(anova(resal.null,resal_fdc, test="Chisq"))

#AIC values to the list
models[[4]]<-resal_fdc
Modnames <- rbind(Modnames,"Female-based full model (d.c.)")

#Calculating Marginal and Conditional R2
r2_fdc<-r.squaredGLMM(resal_fdc)
R2_al<-rbind(R2_al,r2_fdc)

cat("\n\n\n Categorical core area \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn+durationIGE,
family="binomial", data=factors_original))

#Run the model
resal_fcc=glmer(aggression_level ~
  abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resal_fcc))

cat("\n\n\n\n Comparison of female-based model (full, cc) to null model\n\n")
print(anova(resal.null,resal_fcc, test="Chisq"))

#AIC values to the list
models[[5]]<-resal_fcc
Modnames <- rbind(Modnames,"Female-based full model (c.c.)")

#Calculating Marginal and Conditional R2
r2_fcc<-r.squaredGLMM(resal_fcc)
R2_al<-rbind(R2_al,r2_fcc)
```

```
cat("\n\n Male-based models\n\n")

cat("\n\n Intensity of use \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190
# Random effect: 'dyad', 3 levels.
# Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the
proportion of infants/male is higher (3)
# when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=factors_original))

vif(glm(aggression_level ~ abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190+durationIGE,
family="binomial", data=factors_original))

vif(glm(aggression_level ~ abs_nummales+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=factors_original))

#Run the model (no sex ratio)
resal_miu1=glmer(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190+durationIGE+
(1|dyad), family="binomial", data=factors_original)

print(summary(resal_miu1))

cat("\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resal.null,resal_miu1, test="Chisq"))

#AIC values to the list
models[[6]]<-resal_miu1
Modnames <- rbind(Modnames,"Male-based full model (i.u. no sex ratio)")

#Calculating Marginal and Conditional R2
r2_miu1<-r.squaredGLMM(resal_miu1)
R2_al<-rbind(R2_al,r2_miu1)

#Run the model (no pr.infants)
resal_miu2=glmer(aggression_level ~
abs_nummales+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE+
(1|dyad), family="binomial", data=factors_original)

print(summary(resal_miu2))

cat("\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resal.null,resal_miu2, test="Chisq"))

#AIC values to the list
models[[7]]<-resal_miu2
```

```

Modnames <- rbind(Modnames,"Male-based full model (i.u. no pr.infants)")

#Calculating Marginal and Conditional R2
r2_miu2<-r.squaredGLMM(resal_miu2)
R2_al<-rbind(R2_al,r2_miu2)

cat("\n\n Distance to core area \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGEE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190
# Random effect: 'dyad', 3 levels.
# Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the
proportion of infants/male is higher (3)
# when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE,
family="binomial", data=factors_original))

vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea+durationIGE,
family="binomial", data=factors_original))

vif(glm(aggression_level ~
abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE, family="binomial",
data=factors_original))

#Run the model (no sex ratio)
resal_mdc1=glmer(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea+durationIGE+
(1|dyad), family="binomial", data=factors_original)

print(summary(resal_mdc1))

cat("\n\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resal.null,resal_mdc1, test="Chisq"))

#AIC values to the list
models[[8]]<-resal_mdc1
Modnames <- rbind(Modnames,"Male-based full model (d.c. no sex ratio)")

#Calculating Marginal and Conditional R2
r2_mdc1<-r.squaredGLMM(resal_mdc1)
R2_al<-rbind(R2_al,r2_mdc1)

#Run the model (no pr.infants)
resal_mdc2=glmer(aggression_level ~
abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE+
(1|dyad), family="binomial", data=factors_original)

```

```
print(summary(resal_mdc2))

cat("\n\n\n Comparison of male-based model (d.c. no pr.infants) to null model\n\n")
print(anova(resal.null,resal_mdc2, test="Chisq"))

#AIC values to the list
models[[9]]<-resal_mdc2
Modnames <- rbind(Modnames,"Male-based full model (d.c. no pr.infants)")

#Calculating Marginal and Conditional R2
r2_mdc2<-r.squaredGLMM(resal_mdc2)
R2_al<-rbind(R2_al,r2_mdc2)


cat("\n Categorical distance to core \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGEE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the
proportion of infants/male is higher (3)
# when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn+durationIGE,
family="binomial", data=factors_original))

vif(glm(aggression_level ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+durationIGE,
family="binomial", data=factors_original))

vif(glm(aggression_level ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+durationIGE,
family="binomial", data=factors_original))


#Run the model (no sex ratio)
resal_mcc1=glmer(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+durationIGE+
(1|dyad), family="binomial", data=factors_original)

print(summary(resal_mcc1))

cat("\n\n\n Comparison of male-based model (c.c. no sex ratio) to null model\n\n")
print(anova(resal.null,resal_mcc1, test="Chisq"))

#AIC values to the list
models[[10]]<-resal_mcc1
Modnames <- rbind(Modnames,"Male-based full model (c.c. no sex ratio)")

#Calculating Marginal and Conditional R2
```

```

r2_mcc1<-r.squaredGLMM(resal_mcc1)
R2_al<-rbind(R2_al,r2_mcc1)

#Run the model (cc, no pr.infants)
resal_mcc2=glmer(aggression_level ~
  abs_nummales+abs_swfempermale+abs_sexratio+core_yn+durationIGE++
  (1|dyad), family="binomial", data=factors_original)

print(summary(resal_mcc2))

cat("\n\n Comparison of male-based model (c.c., no pr.infants) to null model\n\n")
print(anova(resal.null,resal_mcc2, test="Chisq"))

#AIC values to the list
models[[11]]<-resal_mcc2
Modnames <- rbind(Modnames,"Male-based full model (c.c. no pr.infants)")

#Calculating Marginal and Conditional R2
r2_mcc2<-r.squaredGLMM(resal_mcc2)
R2_al<-rbind(R2_al,r2_mcc2)

#####
#####
#####
#####
cat("\n\n SUMMARY RESULTS \n\n")
####                                #####
#####
#####

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al

#Calculating evidence ratio ( How many times the model.high is more likely than model.low; is to know how well
supported each one is)
aictab<-aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictab, model.high = "top", model.low = "second.ranked")
evidence(aictab, model.high = "top", model.low = "Male-based full model (d.c. no pr.infants)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (c.c. no sex ratio)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (c.c. no pr.infants)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (i.u. no sex ratio)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (i.u. no pr.infants)")
evidence(aictab, model.high = "top", model.low = "Empty null model")
evidence(aictab, model.high = "top", model.low = "Female-based full model (d.c.)")
evidence(aictab, model.high = "top", model.low = "Female-based full model (c.c.)")
evidence(aictab, model.high = "top", model.low = "Female-based full model (i.u.)")

```

```
#The null model is the best of the set

sjp.glmer(resal.null, type="pred", facet.grid=FALSE, vars="durationIGE",
  geom.colors = "bw",show.ci=TRUE)
sjp.glmer(resal_mdc1, type="pred", facet.grid=FALSE, vars="abs_nummales",
  geom.colors = "bw",show.ci=TRUE)

#model averaging
av<-(model.avg(models, beta = c("none", "sd", "partial.sd")))
topmodels<-get.models(av, subset=delta<2)
summary(model.avg(topmodels, beta = c("none", "sd", "partial.sd")))

confint((model.avg(topmodels, beta = c("none", "sd", "partial.sd"))))

cat("\n\n\n\n Is the best model of the previous chapter better than the best of this one? \n\n\n\n")

#Run the model
resal_gs=glmer(aggression_level ~
  abs_groupsize+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resal_gs))

cat("\n\n\n Comparison of group size Model to null model\n\n")
print(anova(resal.null,resal_gs, test="Chisq"))

sjp.glmer(resal_gs, type="pred", facet.grid=FALSE, vars="durationIGE",
  geom.colors = "bw",show.ci=TRUE)
sjp.glmer(resal_gs, type="pred", facet.grid=FALSE, vars="abs_groupsize",
  geom.colors = "bw",show.ci=TRUE)

#Adding result to AIC list
models[[12]]<-resal_gs
Modnames <- rbind(Modnames,"Group size model")

#Calculating R2
r2_gs<-(r.squaredGLMM(resal_gs))
R2_al<-rbind(R2_al,r2_gs)

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al

#Calculating evidence ratio ( How many times the model.high is more likely than model.low; is to know how well
supported each one is)
aictab<-aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictab, model.high = "top", model.low = "second.ranked")
evidence(aictab, model.high = "top", model.low = "Male-based full model (d.c. no sex ratio)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (d.c. no pr.infants)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (c.c. no sex ratio)")
```

```
evidence(aictab, model.high = "top", model.low = "Male-based full model (c.c. no pr.infants)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (i.u. no sex ratio)")
evidence(aictab, model.high = "top", model.low = "Male-based full model (i.u. no pr.infants)")
evidence(aictab, model.high = "top", model.low = "Empty null model")
evidence(aictab, model.high = "top", model.low = "Female-based full model (d.c.)")
evidence(aictab, model.high = "top", model.low = "Female-based full model (c.c.)")
evidence(aictab, model.high = "top", model.low = "Female-based full model (i.u.)")

##Post-hoc analyses

cat("\n\n\n Since group size and duration is the best model, could a model including only the number of
females or males being better than it? \n\n\n ")
#Male model
resal_m=glmer(aggression_level ~
              abs_nummales+duration|GE+
              (1|dyad), family="binomial", data=factors_original)

print(summary(resal_m))

cat("\n\n\n Comparison of male model to null model\n\n\n ")
print(anova(resal.null,resal_m, test="Chisq"))

#AIC values to the list
models[[13]]<-resal_m
Modnames <- rbind(Modnames,"No.males model")

#Calculating Marginal and Conditional R2
r2_m<-r.squaredGLMM(resal_m)
R2_al<-rbind(R2_al,r2_m)

#Female model
resal_f=glmer(aggression_level ~
              abs_numfemales+duration|GE+
              (1|dyad), family="binomial", data=factors_original)

print(summary(resal_f))

cat("\n\n\n Comparison of male model to null model\n\n\n ")
print(anova(resal.null,resal_f, test="Chisq"))

#AIC values to the list
models[[14]]<-resal_f
Modnames <- rbind(Modnames,"No.females model ")

#Calculating Marginal and Conditional R2
r2_f<-r.squaredGLMM(resal_f)
R2_al<-rbind(R2_al,r2_f)

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al

#Calculating evidence ratio
aictab<-aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
```

```
evidence(aictab, model.high = "top", model.low = "second.ranked")
evidence(aictab, model.high = "top", model.low = "No.males model")
evidence(aictab, model.high = "top", model.low = "Null model")

#What if we retain only the variables that the best male models had in common?

resal_ms=glmer(aggression_level ~
  abs_nummales+abs_swfempermale+durationIGE+
  (1|dyad), family="binomial", data=factors_original)

print(summary(resal_ms))

cat("\n\n\n Comparison of male model to null model\n\n")
print(anova(resal.null,resal_ms, test="Chisq"))

#AIC values to the list
models[[15]]<-resal_m
Modnames <- rbind(Modnames,"No.malessw model")

#Calculating Marginal and Conditional R2
r2_ms<-r.squaredGLMM(resal_ms)
R2_al<-rbind(R2_al,r2_ms)

aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al

cat("\n\n\n Is contact aggression more likely when both sexes are aggressive than when only one is? \n\n\n\n")
#sexes and contact aggression
cag<-read.csv("factors_originalv1.csv")

missingrows = is.na(cag$aggression_level)
cag= cag[!missingrows,]
missingrows = is.na(cag$aggression_yn)
cag= cag[!missingrows,]
missingrows = is.na(cag$cat_aggression)
cag= cag[!missingrows,]
cag= cag[cag$cat_aggression!="n",]

resal_sx=glmer(aggression_level ~
  cat_aggression+durationIGE+
  (1|dyad), family="binomial", data=cag)

print(summary(resal_sx))

resalnull=glmer(aggression_level ~
  +durationIGE+(1|dyad), family="binomial", data=cag)

cat("\n\n\n Comparison of sexes model to null model\n\n")
print(anova(resalnull,resal_sx, test="Chisq"))

sjp.glmer(resal_sx, type="pred", facet.grid=FALSE, vars="cat_aggression",
  geom.colors = "bw",show.ci=TRUE)
```



```
(tab<-table(cag$cat_aggression,cag$aggression_level))
(tabsx<-rbind(tab["m",],tab["f",], tab["im",],tab["b",]))#Eliminating the one with no observation( I don't know
why the other thing dint work...arg!)
```

```
chisq.test(tabsx)
```

```
tb <- matrix(c(36,31,2,2,28,8),ncol=2,byrow=TRUE)
colnames(tb) <- c("Non-contact aggression","Contact aggression")
rownames(tb) <- c("Both", "Female","Male")
(tb <- as.table(tb))
```

```
chisq.test(tb)
```

```
#Comparing both+female to male
tb2 <- matrix(c(38,33, 28,8),ncol=2,byrow=TRUE)
colnames(tb2) <- c("Non-contact aggression","Contact aggression")
rownames(tb2) <- c("Both","Male")
(tb2 <- as.table(tb2))
```

```
chisq.test(tb2)# X2 test of independence
```

```
cat("\n\n\n\n\n What if we eliminate pb1r2?? \n\n\n")
```

```
nopb1r2<-factors_original[factors_original$dyad!="pb1r2",]
```

```
cat("\n\n\n\n\n Checking potential control variables \n\n\n\n\n")
#Empty null model
```

```
resal2.null0=glmer(aggression_level ~ 1+ (1| dyad), family="binomial", data=nopb1r2)
```

```
#AIC values to the list
models2<-list()
models2[[1]]<-resal2.null0
Modnames2 <- "Empty null model"
```

```
#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null0<-r.squaredGLMM(resal2.null0)
R2_al<-r2_null0
```

```
cat("\n\n\ Checking potential control variables: Duration and number of observers \n\n")
```

```
resal2_cv=glmer(aggression_level ~ durationIGE+num_obs+(1| dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resal2_cv))
```

```

#Comparison between the null model and the model with potential control variables
print(anova(resal2.null0,resal2_cv, test="Chisq"))
#Duration was significant and too was the full model; duration will be used as control variable

resal2.null=glmer(aggression_level ~ durationIGE+(1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2.null))

#Comparison between the null model and the model with duration as a fixed factor
print(anova(resal2.null0,resal2.null, test="Chisq"))

#AIC values to the list
models2[[2]]<-resal2.null
Modnames2 <- rbind(Modnames2, "Null model")

#Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
r2_null<-r.squaredGLMM(resal2.null)
R2_al<-rbind(R2_al,r2_null)

cat("\n\n\n Female-based models2 \n\n\n")

cat("\n\n\n Intensity of use of space \n\n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=nopb1r2))

#Run the model
resal2_fud=glmer(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_UD190+durationIGE+
(1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_fud))

cat ("\n\n\n\n Comparison of female-based model (full, iu) to null model\n\n\n")

print(anova(resal2.null,resal2_fud, test="Chisq"))

#AIC values to the list
models2[[3]]<-resal2_fud
Modnames2 <- rbind(Modnames2,"Female-based full model (i.u.)")

```

```

#Calculating Marginal and Conditional R2
r2_fud<-r.squaredGLMM(resal2_fud)
R2_al<-rbind(R2_al,r2_fud)

cat("\n\n Distance to core area \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distance to core
area
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea+durationIGE,
family="binomial", data=nopb1r2))

#Run the model
resal2_fdc=glmer(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+abs_distancetocorearea+durationIGE+
(1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_fdc))

cat ("\n\n\n Comparison of female-based model (full, dc) to null model\n\n")

print(anova(resal2.null,resal2_fdc, test="Chisq"))

#AIC values to the list
models2[[4]]<-resal2_fdc
Modnames2 <- rbind(Modnames2,"Female-based full model (d.c.)")

#Calculating Marginal and Conditional R2
r2_fdc<-r.squaredGLMM(resal2_fdc)
R2_al<-rbind(R2_al,r2_fdc)

cat("\n\n Categorical core area \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# hypothesis: Level of aggression would increase (1) when groups have a more similar number of females,(2)
when the contest
#occurred closer to one of its core areas while farther from the opponent's core areas opponent (3) when the
proportion of infants/female
# is similar (4) when the proportion of fertile females/female is similar (5) when the sex ratios (f:m) is similar

```

```
#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn+durationIGE,
family="binomial", data=nopb1r2))

#Run the model
resal2_fcc=glmer(aggression_level ~
abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_sexratio+core_yn+durationIGE+
(1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_fcc))

cat("\n\n\n Comparison of female-based model (full, cc) to null model\n\n\n")
print(anova(resal2.null,resal2_fcc, test="Chisq"))

#AIC values to the list
models2[[5]]<-resal2_fcc
Modnames2 <- rbind(Modnames2,"Female-based full model (c.c.)")

#Calculating Marginal and Conditional R2
r2_fcc<-r.squaredGLMM(resal2_fcc)
R2_al<-rbind(R2_al,r2_fcc)

cat("\n\n\n Male-based models2\n\n\n")

cat("\n\n\n Intensity of use \n\n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGEE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190
# Random effect: 'dyad', 3 levels.
# Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the
proportion of infants/male is higher (3)
# when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=nopb1r2))

vif(glm(aggression_level ~ abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190+durationIGE,
family="binomial", data=nopb1r2))

vif(glm(aggression_level ~ abs_nummales+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE,
family="binomial", data=nopb1r2))

#Run the model (no sex ratio)
resal2_miu1=glmer(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_UD190+durationIGE+
(1|dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resal2_miu1))

cat("\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resal2.null,resal2_miu1, test="Chisq"))

#AIC values to the list
models2[[6]]<-resal2_miu1
Modnames2 <- rbind(Modnames2,"Male-based full model (i.u. no sex ratio)")

#Calculating Marginal and Conditional R2
r2_miu1<-r.squaredGLMM(resal2_miu1)
R2_al<-rbind(R2_al,r2_miu1)

#Run the model (no pr.infants)
resal2_miu2=glmer(aggression_level ~
  abs_nummales+abs_swfempermale+abs_sexratio+abs_UD190+durationIGE+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_miu2))

cat("\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resal2.null,resal2_miu2, test="Chisq"))

#AIC values to the list
models2[[7]]<-resal2_miu2
Modnames2 <- rbind(Modnames2,"Male-based full model (i.u. no pr.infants)")

#Calculating Marginal and Conditional R2
r2_miu2<-r.squaredGLMM(resal2_miu2)
R2_al<-rbind(R2_al,r2_miu2)

cat("\n\n Distance to core area \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGEE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_UD190
# Random effect: 'dyad', 3 levels.
# Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the
proportion of infants/male is higher (3)
# when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE,
family="binomial", data=nopb1r2))

vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea+durationIGE,
family="binomial", data=nopb1r2))

vif(glm(aggression_level ~
abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE, family="binomial",
data=nopb1r2))
```

```
#Run the model (no sex ratio)
resal2_mdc1=glmer(aggression_level ~
  abs_nummales+abs_numinfpermale+abs_swfempermale+abs_distancetocorearea+durationIGE+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_mdc1))

cat("\n\n\n Comparison of male-based model 1 (full) to null model\n\n")
print(anova(resal2.null,resal2_mdc1, test="Chisq"))

#AIC values to the list
models2[[8]]<-resal2_mdc1
Modnames2 <- rbind(Modnames2,"Male-based full model (d.c. no sex ratio)")

#Calculating Marginal and Conditional R2
r2_mdc1<-r.squaredGLMM(resal2_mdc1)
R2_al<-rbind(R2_al,r2_mdc1)

#Run the model (no pr.infants)
resal2_mdc2=glmer(aggression_level ~
  abs_nummales+abs_swfempermale+abs_sexratio+abs_distancetocorearea+durationIGE+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_mdc2))

cat("\n\n\n Comparison of male-based model (d.c. no pr.infants) to null model\n\n")
print(anova(resal2.null,resal2_mdc2, test="Chisq"))

#AIC values to the list
models2[[9]]<-resal2_mdc2
Modnames2 <- rbind(Modnames2,"Male-based full model (d.c. no pr.infants)")

#Calculating Marginal and Conditional R2
r2_mdc2<-r.squaredGLMM(resal2_mdc2)
R2_al<-rbind(R2_al,r2_mdc2)

cat("\n\n Categorical distance to core \n\n")
# Response: aggression_level (binary,1=Contact-Aggression IGEE, 0=Non-contact aggression IGE)
# Control variables: durationIGE
# Fixed effect: abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn
# Random effect: 'dyad', 3 levels.
# Hypothesis: Level of aggression would increase (1) when groups were more similar in size, (2) when the
proportion of infants/male is higher (3)
# when the proportion of fertile females/male is smaller (4) No effect on the sex ratio

#Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
```

```
vif(glm(aggression_level ~
abs_nummales+abs_numinfpermale+abs_swfempermale+abs_sexratio+core_yn+durationIGE,
family="binomial", data=nopb1r2))

vif(glm(aggression_level ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+durationIGE,
family="binomial", data=nopb1r2))

vif(glm(aggression_level ~ abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+durationIGE,
family="binomial", data=nopb1r2))

#Run the model (no sex ratio)
resal2_mcc1=glmer(aggression_level ~
  abs_nummales+abs_numinfpermale+abs_swfempermale+core_yn+durationIGE+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_mcc1))

cat("\n\n\n Comparison of male-based model (c.c. no sex ratio) to null model\n\n")
print(anova(resal2.null,resal2_mcc1, test="Chisq"))

#AIC values to the list
models2[[10]]<-resal2_mcc1
Modnames2 <- rbind(Modnames2,"Male-based full model (c.c. no sex ratio)")

#Calculating Marginal and Conditional R2
r2_mcc1<-r.squaredGLMM(resal2_mcc1)
R2_al<-rbind(R2_al,r2_mcc1)

#Run the model (cc, no pr.infants)
resal2_mcc2=glmer(aggression_level ~
  abs_nummales+abs_swfempermale+abs_sexratio+core_yn+durationIGE++
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resal2_mcc2))

cat("\n\n\n Comparison of male-based model (c.c., no pr.infants) to null model\n\n")
print(anova(resal2.null,resal2_mcc2, test="Chisq"))

#AIC values to the list
models2[[11]]<-resal2_mcc2
Modnames2 <- rbind(Modnames2,"Male-based full model (c.c. no pr.infants)")

#Calculating Marginal and Conditional R2
r2_mcc2<-r.squaredGLMM(resal2_mcc2)
R2_al<-rbind(R2_al,r2_mcc2)
```

```
#####
cat("\n\n\n SUMMARY RESULTS \n\n\n")
#####
```

```
aictab(cand.set=models2, modnames = Modnames2 , second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al
```

```
aictab2<-aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictab2, model.high = "top", model.low = "second.ranked")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (d.c. no pr.infants)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (d.c. no sex ratio)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (c.c. no sex ratio)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (i.u. no pr.infants)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (i.u. no sex ratio)")
evidence(aictab2, model.high = "top", model.low = "Empty null model")
evidence(aictab2, model.high = "top", model.low = "Female-based full model (d.c.)")
evidence(aictab2, model.high = "top", model.low = "Female-based full model (c.c.)")
evidence(aictab2, model.high = "top", model.low = "Female-based full model (i.u.)")
```

```
av2<-(model.avg(models2, beta = c("none", "sd", "partial.sd")))
topmodels2<-get.models(av2, subset=delta<2)
summary(model.avg(topmodels2, beta = c("none", "sd", "partial.sd")))
```

```
confint((model.avg(topmodels, beta = c("none", "sd", "partial.sd"))))
```

```
cat("\n\n\n\n\n Is the best model of the previous chapter better than the best of this one? \n\n\n\n\n")
```

```
#Run the model
resal2_gs=glmer(aggression_level ~
  abs_groupsize+duration|GE+
  (1|dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resal2_gs))
```

```
cat("\n\n\n\n Comparison of group size Model to null model\n\n\n")
print(anova(resal2.null,resal2_gs, test="Chisq"))
```

```
#Adding result to AIC list
models2[[12]]<-resal2_gs
Modnames2 <- rbind(Modnames2,"Group size model")
```

```
#Calculating R2
r2_gs<-(r.squaredGLMM(resal2_gs))
R2_al<-rbind(R2_al,r2_gs)
```



```
aictab(cand.set=models2, modnames = Modnames2 , second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al
```

```
aictab2<-aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictab2, model.high = "top", model.low = "second.ranked")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (c.c. no pr.infants)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (d.c. no pr.infants)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (d.c. no sex ratio)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (c.c. no sex ratio)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (i.u. no pr.infants)")
evidence(aictab2, model.high = "top", model.low = "Male-based full model (i.u. no sex ratio)")
evidence(aictab2, model.high = "top", model.low = "Empty null model")
evidence(aictab2, model.high = "top", model.low = "Female-based full model (d.c.)")
evidence(aictab2, model.high = "top", model.low = "Female-based full model (c.c.)")
evidence(aictab2, model.high = "top", model.low = "Female-based full model (i.u.)")
```

```
##Post-hoc analyses
```

```
cat("\n\n\n Since group size and duration is the best model, could a model including only the number of
females or males being better than it? \n\n\n ")
```

```
#Male model
```

```
resal_m2=glmer(aggression_level ~
              abs_nummales+duration|GE+
              (1|dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resal_m2))
```

```
cat("\n\n\n Comparison of male model to null model\n\n")
print(anova(resal2.null,resal_m2, test="Chisq"))
```

```
#AIC values to the list
```

```
models2[[13]]<-resal_m2
Modnames2 <- rbind(Modnames2,"No.males model2")
```

```
#Calculating Marginal and Conditional R2
```

```
r2_m2<-r.squaredGLMM(resal_m2)
R2_al<-rbind(R2_al,r2_m2)
```

```
#Female model
```

```
resal_f2=glmer(aggression_level ~
              abs_numfemales+duration|GE+
              (1|dyad), family="binomial", data=nopb1r2)
```

```
print(summary(resal_f2))
```

```
cat("\n\n\n Comparison of male model to null model\n\n")
print(anova(resal2.null,resal_f2, test="Chisq"))
```

```
#AIC values to the list
```

```
models2[[14]]<-resal_f2
Modnames2 <- rbind(Modnames2,"No.females model 2")
```

```
#Calculating Marginal and Conditional R2
```

```
r2_f2<-r.squaredGLMM(resal_f2)
```

```
R2_al<-rbind(R2_al,r2_f2)

aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al

#Calculating evidence ratio
aictab<-aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
evidence(aictab, model.high = "top", model.low = "second.ranked")
evidence(aictab, model.high = "top", model.low = "No.females model 2")
evidence(aictab, model.high = "top", model.low = "Null model")

#What if we retain only the variables that the best male models had in common?

resal_ms2=glmer(aggression_level ~
  abs_nummales+abs_swfempermale+durationIGE+
  (1|dyad), family="binomial", data=nopb1r2)

print(summary(resal_ms2))

cat("\n\n\n Comparison of male model to null model\n\n")
print(anova(resal2.null,resal_ms2, test="Chisq"))

#AIC values to the list
models2[[15]]<-resal_ms2
Modnames2 <- rbind(Modnames2,"No.malessw model")

#Calculating Marginal and Conditional R2
r2_ms2<-r.squaredGLMM(resal_ms2)
R2_al<-rbind(R2_al,r2_ms2)

aictab(cand.set=models2, modnames = Modnames2, second.ord = TRUE, nobs = NULL, sort = TRUE)
R2_al
```

3.1.6. EXPLORATION OF HOW REPRODUCTIVE STRATEGIES PROXIES AFFECT THE DURATION OF INTERGROUP ENCOUNTERS

```
#####DURATIION OF IGE EXPLORATION###
install.packages("ggplot2")
library(ggplot2)
install.packages("car")#Package to check regression "quality"
library(car)
install.packages("ppcor")
library(ppcor)
library(lme4)

setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()
```

```

dir()

## Upload data (when involved in parenthesis, the assigned variable/dataframe/etc is also printed in addition to
be assigned)

factors_original<-read.csv("factors_originalv1.csv")

####Convert variables to the appropriate format
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$abs_numfemales<- as.numeric(factors_original$abs_numfemales)
factors_original$abs_nummales<- as.numeric(factors_original$abs_nummales)
factors_original$abs_numinfperfem<- as.numeric(factors_original$abs_numinfperfem)
factors_original$abs_numinfpermale<- as.numeric(factors_original$abs_numinfpermale)
factors_original$abs_swfemperfem<- as.numeric(factors_original$abs_swfemperfem)
factors_original$abs_swfempermale<- as.numeric(factors_original$abs_swfempermale)
factors_original$abs_sexratio<- as.numeric(factors_original$abs_sexratio)


#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison
cannot be made)
missingrows = is.na(factors_original$ abs_nummales)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numfemales)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numinfperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_numinfpermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_swfemperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$abs_sexratio)
factors_original= factors_original[!missingrows,]

nopb1r2<-factors_original[factors_original$dyad!="pb1r2",]

table(factors_original$cat_aggression, factors_original$contact_aggresion)

cat("\n\n\n\n\n\n\n\n Duration data distribution \n\n\n\n\n\n\n\n")

shapiro.test(factors_original$durationIGE)# The hypothesis that the sample has a normal distribution cannot be
rejected (p>0.05)

install.packages("fitdistrplus")##To find what distribution the data have
library(fitdistrplus)

```

```
install.packages("logspline")##To find data distribution
library(logspline)

durat<-factors_original$durationlGE
summary(durat)

descdist(durat, discrete = FALSE)#This functions allow us to know what possible distribution/s the data could
follow (Cullen & Frey Graph)
# Beta distribution seems to appropriate one.However, GLMMs wit beta dis cannot be run with lme4 but with
glmmADMB, for which little
#information is available and is advanced, out of the scope of this project
```

```
####Splitting the data per dyad
pb1r1<-(factors_original[factors_original$dyad=="pb1r1",])
r1r2<-(factors_original[factors_original$dyad=="r1r2",])
pb1r2<-(factors_original[factors_original$dyad=="pb1r2",])

cat("\n\n\n\n\n\n\n Partial correlations for PB1-R1\n\n\n\n\n\n\n")

##Duration & No.females
durf_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_numfemales)
pcor(durf_pb1r1, method="pearson")
pcor(durf_pb1r1, method="spearman")

##Graph
plot(x = pb1r1$abs_numfemales,
     y = pb1r1$durationIGE,
     xlab = "Absolute No.females (No.Individuals)",
     ylab = "Duration (min)")

M0 <- lm(durationIGE~ abs_numfemales,
        data = pb1r1)
abline(M0, lwd = 3)
summary(M0)
```

```
##Duration & No.males
durm_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_nummales)
pcor(durm_pb1r1, method="pearson")
pcor(durm_pb1r1, method="spearman")

##Graph
plot(x = pb1r1$abs_nummales,
     y = pb1r1$durationIGE,
     xlab = "Absolute between-group difference in the number of males (No.Individuals)",
     ylab = "Duration (min)")

M0 <- lm(durationIGE~ abs_nummales,
         data = pb1r1)
abline(M0, lwd = 3)
```

```
##Duration & Pr.infants per female
durif_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_numinfperfem)
pcor(durif_pb1r1, method="pearson")
pcor(durif_pb1r1, method="spearman")
```

```
##Graph
plot(x = pb1r1$abs_numinfperfem,
     y = pb1r1$durationIGE,
     xlab = "Absolute No.infants per female (No.Individuals)",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_numinfperfem,
         data = pb1r1)
abline(M0, lwd = 3)
```

```
##Duration & Pr.infants per male
durim_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_numinfpermale)
pcor(durim_pb1r1, method="pearson")
pcor(durim_pb1r1, method="spearman")
```

```
##Graph
plot(x = pb1r1$abs_numinfpermale,
     y = pb1r1$durationIGE,
     xlab = "Absolute No.infants per male ",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_numinfpermale,
         data = pb1r1)
abline(M0, lwd = 3)
```

```
##Duration & No.fertile females per female
durisf_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_swfemperfem )
pcor(durisf_pb1r1, method="pearson")
pcor(durisf_pb1r1, method="spearman")
```

```
##Graph
plot(x = pb1r1$abs_swfemperfem ,
     y = pb1r1$durationIGE,
     xlab = "Absolute No.fertile females per female ",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_swfemperfem ,
         data = pb1r1)
abline(M0, lwd = 3)
```

```
##Duration & No.fertile females per male
durimsf_pb1r1<-data.frame(pb1r1$durationIGE,pb1r1$abs_swfempermale )
```



```
##Duration & No.males
durm_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_nummales)
pcor(durm_r1r2, method="pearson")
pcor(durm_r1r2, method="spearman")
```

```
##Graph
plot(x = r1r2$abs_nummales,
     y = r1r2$durationIGE,
     xlab = "Absolute No.males (No.Individuals)",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_nummales,
         data = r1r2)
abline(M0, lwd = 3)
```

```
##Duration & Pr.infants per female
durif_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_numinfperfem)
pcor(durif_r1r2, method="pearson")
pcor(durif_r1r2, method="spearman")
```

```
##Graph
plot(x = r1r2$abs_numinfperfem,
     y = r1r2$durationIGE,
     xlab = "Absolute No.infants per female (No.Individuals)",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_numinfperfem,
         data = r1r2)
abline(M0, lwd = 3)
```

```
##Duration & Pr.infants per male
durim_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_numinfpermale)
pcor(durim_r1r2, method="pearson")
pcor(durim_r1r2, method="spearman")
```

```
##Graph
plot(x = r1r2$abs_numinfpermale,
     y = r1r2$durationIGE,
     xlab = "Absolute No.infants per male ",
     ylab = "Duration (min)")
```

```
M0 <- lm(durationIGE~ abs_numinfpermale,
         data = r1r2)
abline(M0, lwd = 3)
```

```
##Duration & No.fertile females per female
durisf_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_swfemperfem )
pcor(durisf_r1r2, method="pearson")
pcor(durisf_r1r2, method="spearman")
```

```
##Graph
plot(x = r1r2$abs_swfemperfem ,
     y = r1r2$durationIGE,
     xlab = "Absolute No.fertile females per female ",
     ylab = "Duration (min)")

M0 <- lm(durationIGE~ abs_swfemperfem ,
         data = r1r2)
abline(M0, lwd = 3)

##Duration & No.fertile females per male
durifm_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_swfempermale )
pcor(durifm_r1r2, method="pearson")
pcor(durifm_r1r2, method="spearman")

##Graph
plot(x = r1r2$abs_swfempermale ,
     y = r1r2$durationIGE,
     xlab = "Absolute No.fertile females per male",
     ylab = "Duration (min)")

M0 <- lm(durationIGE~ abs_swfempermale ,
         data = r1r2)
abline(M0, lwd = 3)

##Duration & Absolute sex ratio
dursr_r1r2<-data.frame(r1r2$durationIGE,r1r2$abs_sexratio)
pcor(dursr_r1r2, method="pearson")
pcor(dursr_r1r2, method="spearman")

##Graph
plot(x = r1r2$abs_sexratio,
     y = r1r2$durationIGE,
     xlab = "Absolute sex ratio",
     ylab = "Duration (min)")

M0 <- lm(durationIGE~ abs_sexratio,
         data = r1r2)
abline(M0, lwd = 3)

##PB1-R2
pb1r2$abs_numfemales
pb1r2$abs_nummales
pb1r2$abs_numinfperfem
pb1r2$abs_numinfpermale
pb1r2$abs_swfemperfem
pb1r2$abs_swfempermale
pb1r2$abs_sexratio
```



```
ggplot(factors_original, aes(x=aggression_yn,y=durationIGE))+  
  geom_boxplot()
```

```
ggplot(factors_original, aes(x=aggression_yn,y=durationIGE))+  
  geom_boxplot()+  
  facet_wrap(~dyad)
```

```
cat("\n Residuals VS Fitted values (https://onlinecourses.science.psu.edu/stat501/node/36 [Accessed 11th Sep  
2017] n\n")  
# Here are the characteristics of a well-behaved residual vs. fits plot and what they suggest about the  
appropriateness of the simple linear regression model:  
# The residuals "bounce randomly" around the 0 line. This suggests that the assumption that the relationship is  
linear is reasonable.  
# The residuals roughly form a "horizontal band" around the 0 line. This suggests that the variances of the error  
terms are equal.  
# No one residual "stands out" from the basic random pattern of residuals. This suggests that there are no  
outliers.
```

```
cat("\n\n\n\n What if we remove the 2 IGEs PB1-R2?\n\n\n\n")
```

```
##Partial correlation
```

```
durgs<-data.frame(nopb1r2$durationIGE,nopb1r2$abs_groupsize)  
pcor(durgs, method="pearson")  
cor(nopb1r2$durationIGE,nopb1r2$abs_groupsize)
```

```
##Graph
```

```
plot(x = nopb1r2$abs_groupsize,  
     y = nopb1r2$durationIGE,  
     xlab = "Absolute group size",  
     ylab = "Duration")
```

```
M0 <- lm(durationIGE~abs_groupsize, data = nopb1r2)  
abline(M0, lwd = 3)
```

```
summary(M0)  
plot(M0)
```

```
cat("\n\n\n\n\n\n\n\n Duration and use of space difference\n\n\n\n\n\n\n\n")
```

```
##Partial correlation
```

```
durud<-data.frame(factors_original$durationIGE,factors_original$abs_UD190)
```

```

pcor(durud, method="pearson")

##Graph
plot(x = factors_original$abs_UD190,
     y = factors_original$durationIGE,
     xlab = "Absolute use of space",
     ylab = "Duration")

M0 <- lm(durationIGE~ abs_UD190,
factors_original)
abline(M0, lwd = 3)

summary(M0)

plot(M0)

cat("\n\n\n\n\n\n\n Duration and distance to core \n\n\n\n\n\n\n")

##Partial correlation

durds<-data.frame(factors_original$durationIGE,factors_original$abs_distancetocorearea)
pcor(durds, method="pearson")

##Graph
plot(x = factors_original$abs_distancetocorearea,
     y = factors_original$durationIGE,
     xlab = "Absolute distance to core",
     ylab = "Duration")

M0 <- lm(durationIGE~abs_distancetocorearea, factors_original)
abline(M0, lwd = 3)

summary(M0)

plot(M0)

cat("\n\n\n\n\n\n\n Duration and dyad \n\n\n\n\n\n\n")

ggplot(factors_original, aes(x=durationIGE))+
  geom_histogram()+
  facet_wrap(~dyad)

boxplot(durationIGE~ dyad,
        data = factors_original)

summary(factors_original$durationIGE[factors_original$dyad=="pb1r1"])
summary(factors_original$durationIGE[factors_original$dyad=="r1r2"])
summary(factors_original$durationIGE[factors_original$dyad=="pb1r2"])

```

```
cat("\n\n\n\n\n\n\n Duration and decided vs undecided encounters \n\n\n\n\n\n\n\n")
```

```
ggplot(factors_original, aes(x=durationIGE))+  
  geom_histogram()+  
  facet_wrap(~decided_undecided)
```

```
boxplot(durationIGE~ decided_undecided,  
  data = factors_original)
```

```
summary(factors_original$durationIGE[factors_original$decided_undecided=="1"])  
summary(factors_original$durationIGE[factors_original$decided_undecided=="0"])
```

```
cat("\n\n\n\n\n\n\n Duration and aggression per sex \n\n\n\n\n\n\n\n")
```

```
## Upload data (when involved in parenthesis, the assigned variable/dataframe/etc is also printed in addition to  
be assigned)
```

```
factors_original<-read.csv("factors_originalv1.csv")
```

```
missingrows = is.na(factors_original$cat_aggression)  
factors_original= factors_original[!missingrows,]  
missingrows = is.na(factors_original$aggression_m)  
factors_original= factors_original[!missingrows,]  
missingrows = is.na(factors_original$aggression_f)  
factors_original= factors_original[!missingrows,]
```

```
factors_original<-factors_original[factors_original$cat_aggression!="NA",]
```

```
table(factors_original$cat_aggression)
```

```
#Comparison between durations
```

```
n_data<-factors_original[factors_original$cat_aggression=="n",]  
n<-n_data$durationIGE  
f_data<-factors_original[factors_original$cat_aggression=="f",]  
f<-f_data$durationIGE  
m_data<-factors_original[factors_original$cat_aggression=="m",]  
m<-m_data$durationIGE  
b_data<-factors_original[factors_original$cat_aggression=="b",]  
b<-b_data$durationIGE
```

```

#All
  kruskal.test(list(n,f,m,b))
#n-f
kruskal.test(list(n,f))
#n-m
kruskal.test(list(n,m))
#n-b
kruskal.test(list(n,b))

#f-m
kruskal.test(list(f,m))

#f-b
kruskal.test(list(f,b))

#m-b
kruskal.test(list(m,b))

table(factors_original$score_yn,
      factors_original$cat_aggression)

boxplot(durationIGE~ cat_aggression,
        data = pb1r1)

#####

####Now by dyad#####

#####

pb1r1<-(factors_original[factors_original$dyad=="pb1r1",])
r1r2<-(factors_original[factors_original$dyad=="r1r2",])
pb1r2<-(factors_original[factors_original$dyad=="pb1r2",])

###PB1-R1
names<-c("Both", "Females", "Males", "None")
boxplot(durationIGE~ cat_aggression,
        data = pb1r1,names=names)

p<-ggplot(pb1r1,aes(cat_aggression, durationIGE))
p+ geom_boxplot()+
  geom_jitter(width = 0.2)+
  labs(x = "Aggression by", y="Duration of IGE (min.)")+
  theme_bw()+
  scale_x_discrete(labels=c("b" = "Both", "f" = "Females", "m" = "Males", "n"="None"))+
  scale_y_continuous(limits = c(0, 700))

```

```

n_data<-pb1r1[pb1r1$cat_aggression=="n",]
n<-n_data$durationIGE
f_data<-pb1r1[pb1r1$cat_aggression=="f",]
f<-f_data$durationIGE
m_data<-pb1r1[pb1r1$cat_aggression=="m",]
m<-m_data$durationIGE
b_data<-pb1r1[pb1r1$cat_aggression=="b",]
b<-b_data$durationIGE
summary(n)
summary(f)
summary(m)
summary(b)

#All
kruskal.test(list(n,f,m,b))
#n-f
kruskal.test(list(n,f))
#n-m
kruskal.test(list(n,m))
#n-b
kruskal.test(list(n,b))

#f-m
kruskal.test(list(f,m))

#f-b
kruskal.test(list(f,b))

#m-b
kruskal.test(list(m,b))

###R1-R2

boxplot(durationIGE~ cat_aggression,
data = r1r2)

table(r1r2$cat_aggression,
r1r2$durationIGE)

p<-ggplot(r1r2,aes(cat_aggression, durationIGE))
p+ geom_boxplot()+
geom_jitter(width = 0.2)+
labs(x = "Aggression by", y="Duration of IGE (min.)")+
theme_bw()+
scale_x_discrete(labels=c("b" = "Both", "f" = "Females", "m" = "Males", "n"="None"))+
scale_y_continuous(limits = c(0, 700))

n_data<-r1r2[r1r2$cat_aggression=="n",]
n<-n_data$durationIGE
f_data<-r1r2[r1r2$cat_aggression=="f",]

```

```
f<-f_data$durationIGE
m_data<-r1r2[r1r2$cat_aggression=="m",]
m<-m_data$durationIGE
b_data<-r1r2[r1r2$cat_aggression=="b",]
b<-b_data$durationIGE

summary(n)
summary(f)
summary(m)
summary(b)

#All
kruskal.test(list(n,f,m,b))
#n-f
kruskal.test(list(n,f))
#n-m
kruskal.test(list(n,m))
#n-b
kruskal.test(list(n,b))

#f-m
kruskal.test(list(f,m))

#f-b
kruskal.test(list(f,b))

#m-b
kruskal.test(list(m,b))

cat("\n\n\n\n\n\n\n\n\n\n Means and such \n\n\n\n\n\n\n\n\n\n")
factors_original<-read.csv("factors_originalv1.csv")
str(factors_original)

#Are all the encounters with aggression longer than those without?
#No, there is some overlap
aggressive_IGEs<-factors_original[factors_original$aggression_yn=="1",]
nonaggressive_IGEs<-factors_original[factors_original$aggression_yn=="0",]
summary(aggressive_IGEs$durationIGE)
summary(nonaggressive_IGEs$durationIGE)

# What about sex-age classess (aggressive encounters without adult participation)

factors_original<-read.csv("factors_originalv1.csv")
missingrows = is.na(factors_original$aggression_yn)
factors_original= factors_original[!missingrows,]
aggressive_IGEs<-factors_original[factors_original$aggression_yn=="1",]

faggressive<-aggressive_IGEs[aggressive_IGEs$cat_aggression=="f",]
```

```

maggressive<-aggressive_IGEs[aggressive_IGEs$cat_aggression=="m",]
noadultsaggressive<-aggressive_IGEs[aggressive_IGEs$cat_aggression=="n",]
baggressive<-aggressive_IGEs[aggressive_IGEs$cat_aggression=="b",]
summary(faggressive$durationIGE)
summary(maggressive$durationIGE)
summary(baggressive$durationIGE)
summary(noadultsaggressive$durationIGE)

# Adding distinction between peaceful encounters and encounters with only immature aggression

aggression<-read.csv("cataggression.csv")
missingrows = is.na(aggression$cat_aggression)
aggression= aggression[!missingrows,]

faggressive<-aggression[aggression$cat_aggression=="f",]
maggressive<-aggression[aggression$cat_aggression=="m",]
peaceful<-aggression[aggression$cat_aggression=="n",]
baggressive<-aggression[aggression$cat_aggression=="b",]
imaggressive<-aggression[aggression$cat_aggression=="im",]
summary(faggressive$durationIGE)
summary(maggressive$durationIGE)
summary(baggressive$durationIGE)
summary(peaceful$durationIGE)
summary(imaggressive$durationIGE)

p<-ggplot(aggression,aes(cat_aggression, durationIGE))
p+ geom_boxplot()+
geom_jitter(width = 0.2)+
labs(x = "Aggression by", y="Duration of IGE (min.)")+
theme_bw()+
scale_x_discrete(labels=c("b" = "Both", "f" = "Females", "m" = "Males", "n"="None", "im"="immatures"))+
scale_y_continuous(limits = c(0, 700))

```

3.2. Models following predicting probability of winning an encounter as in Markham et al. 2012

```

## download packages
# installing/loading the package:
if(!require(installr)) {
  install.packages("installr"); require(installr)} #load / install+load installr

# using the package:
updateR() # This will start the updating process of your R installation.
# It will check for newer versions, and if one is available, will guide you through the decisions you'd need to make.

## download packages
install.packages("lme4")#Package that allows to calculate the glms

```

```
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("ppcor")#To check for correlations between independent variables
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine
```

```
library(lme4)
library(car)
library(ggplot2)
library(modEvA)
library(languageR)
library(ppcor)
library(AICcmodavg)
library(MuMIn)
library(dplyr)
library(sjPlot)
```

```
#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()
```

```
## Upload data
factors_original<-read.csv("factors_originalv1.csv")
```

```
#### Flip the variables for pb1-r1 so R1 is the focal group in all the encounters with decided outcome
```

```
#Checking the original data
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]
```

```
#Flipping pb1-r1 to r1-pb1
factors_original$winner_analysis[ factors_original$dyad=="pb1r1"] <-1-
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_groupsize[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_groupsize[
factors_original$dyad=="pb1r1"]
factors_original$rel_nummales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_nummales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numfemales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numfemales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numinfperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfperfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfpermale[
factors_original$dyad=="pb1r1"]
```



```
factors_original$rel_numswfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numswfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swgs[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swgs[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfemperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfemperfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfempermale[
factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_sexratio[
factors_original$dyad=="pb1r1"]
factors_original$rel_UD190[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_UD190[factors_original$dyad=="pb1r1"]
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"]
```

#Checking that the flipping worked

```
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]
```

###Convert variables to the appropriate format

```
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$winner_analysis<- as.numeric(factors_original$winner_analysis)#If written as factor at this
stage, the flipping goes wrong
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$rel_numfemales<- as.numeric(factors_original$rel_numfemales)
factors_original$rel_nummales<- as.numeric(factors_original$rel_nummales)
factors_original$rel_UD190<- as.numeric(factors_original$rel_UD190)
factors_original$winner_analysis<- as.factor(factors_original$winner_analysis)#Now we can transform it into
factor without problems
```

#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison cannot be made)

```
missingrows = is.na(factors_original$rel_nummales)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numfemales)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numinfperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numinfpermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_swfemperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_sexratio)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$winner_analysis)
factors_original= factors_original[!missingrows,]
```

```
> cat("\n\n\n\n\n\n Checking potential control variables \n\n\n\n\n\n")
)
```

Checking potential control variables

```
> #null model
>
> res.null=glmer(winner_analysis ~ 1+ (1|dyad), family="binomial", data=factors_original)
>
> #AIC values to the list
> models<-list()
> models[[1]]<-res.null
> Modnames <- "null model"
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_null<-r.squaredGLMM(res.null)
The result is correct only if all data used by the model has not changed since model was fitted.
> R2<-r2_null
>
>
> cat("\n\n\n Checking potential control variables: Duration and number of observers \n\n\n")
```

Checking potential control variables: Duration and number of observers

```
>
> res_cv=glmer(winner_analysis ~durationIGE+num_obs+(1|dyad), family="binomial", data=factors_original)
>
> print(summary(res_cv))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ durationIGE + num_obs + (1 | dyad)
Data: factors_original

            AIC      BIC    logLik deviance df.resid
        130.0      140.1     -61.0    122.0        90

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.84259 -0.85489  0.08184  0.85079  1.91944

Random effects:
Groups Name      Variance Std.Dev.
dyad    (Intercept) 0.1797   0.4239
```

```

Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.696607   0.656073  -1.062   0.2883
durationIGE -0.003549   0.002153  -1.648   0.0993 .
num_obs      0.455778   0.279727   1.629   0.1032
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) drtIGE
durationIGE -0.028
num_obs     -0.741 -0.388
>
> #Comparison between the null model and the model with c.v
> print(anova(res.null,res_cv, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_cv:  winner_analysis ~ durationIGE + num_obs + (1 | dyad)
              Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null    2 130.19 135.27 -63.093   126.19
res_cv      4 129.96 140.13 -60.979   121.96 4.2285      2    0.1207
>
>
>
>
>
> #Check that no combination between response and random effects is to
o unfrequent
> table(factors_original$winner_analysis, factors_original$dyad)

      pb1r1 pb1r2 r1r2
0         23      0   24
1         37      0  10
>
>
>
>
> cat("\n\n\n\n\n\n\n\n Female-based model with use of space \n\n\n\n\n\n\n\n\n\n")

```

Female-based model with use of space

>

```

> # Response: winner_analysis (binary, 1=Focal group wins, 0= Focal group loses)
> # Fixed effects: rel_numfemales+rel_numinfperfem+rel_swfemperfem+rel_sexratio+rel_UD190
> # Random effect: 'dyad', 2 levels.
> # Hypothesis: "A group would have increased odds of winning (1) when its number of females was larger than its opponent,
> # (2) when the proportion of infants/female is smaller (3) when the proportion of fertile females/female is smaller
> # (4) when the sex ratios (f:m) is higher than those of the opponent
>
> #Checking co-linearity (values close to 1 are good, over 4 can be problematic)
> vif(glm(winner_analysis ~ rel_numfemales+rel_UD190, family="binomial", data=factors_original))
rel_numfemales    rel_UD190
      1.077043      1.077043
>
> #Run the model
> res_f=glmer(winner_analysis ~
+             rel_numfemales+rel_UD190+
+             (1|dyad), family="binomial", data=factors_original)
>
> print(summary(res_f))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_numfemales + rel_UD190 + (1 | dyad)
Data: factors_original

            AIC      BIC    logLik deviance df.resid
      128.2    138.4    -60.1    120.2      90

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.31558 -0.93042  0.05856  0.84231  1.87649

Random effects:
Groups Name      Variance Std.Dev.
dyad (Intercept) 0.3905   0.6249
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.330269   1.498094  -0.888   0.3746
rel_numfemales  0.147644   0.185442   0.796   0.4259
rel_UD190      0.013819   0.006102   2.265   0.0235 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) rel_nmf
rel_numfmls  -0.942
rel_UD190    -0.139  0.125
>
> cat("\n\n\n Comparison of female-based (full; UD) model to null model\n\n")

```

Comparison of female-based (full; UD) model to null model

```
>
> print(anova(res.null,res_f, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_f: winner_analysis ~ rel_numfemales + rel_UD190 + (1 | dyad)
      Df    AIC    BIC logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 130.19 135.27 -63.093   126.19      2    0.05072 .
res_f     4 128.22 138.40 -60.112   120.22      2    0.05072 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> #AIC values to the list
> models[[2]]<-res_f
> Modnames <- rbind(Modnames, "Female based")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and
> Schielzeth, 2013)
> r2_f<-r.squaredGLMM(res_f)
The result is correct only if all data used by the model has not changed
since model was fitted.
> R2<-rbind(R2,r2_f)
>
>
>
> cat("\n\n\n\n\n\n\n\n Male-based model with UD_190\n\n\n\n\n\n\n\n\n\n")
```

Male-based model with UD_190

```
>
>
>
> cat("\n\n\n\n\n\n\n\n Male-based model 1 \n\n\n")
```

Male-based model 1

```
> #Run full the model
```

```

>
> res_m=glmer(winner_analysis ~ rel_nummales+rel_UD190+
+             (1|dyad), family="binomial", data=factors_origina
1)
>
>
> print(summary(res_m))
Generalized linear mixed model fit by maximum likelihood (Laplace Appr
oximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_nummales + rel_UD190 + (1 | dyad)
Data: factors_original

            AIC      BIC    logLik deviance df.resid
      128.5     138.7     -60.3    120.5        90

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.38499 -0.88085  0.05104  0.81256  1.83520

Random effects:
 Groups Name      Variance Std.Dev.
 dyad    (Intercept) 0.7303   0.8546
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   1.248688   2.660720   0.469   0.6389
rel_nummales -0.232181   0.410610  -0.566   0.5718
rel_UD190      0.013366   0.006117   2.185   0.0289 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) rl_nmm
rel_nummales -0.970
rel_UD190     0.008 -0.019
>
>
> cat("\n\n\n Comparison of male based model (full1) to null model\n\n
")

```

Comparison of male based model (full1) to null model

```

> print(anova(res.null,res_m, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_m: winner_analysis ~ rel_nummales + rel_UD190 + (1 | dyad)
      Df    AIC    BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 130.19 135.27 -63.093   126.19      2    0.05948 .
res_m     4 128.54 138.72 -60.271   120.54  5.6443      2    0.05948 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> #The full model wasn't significant (but almost) so no adj. model is
produced
>
> #AIC values to the list

```

```

> models[[3]]<-res_m
> Modnames <- rbind(Modnames, "Male based")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and
Schielzeth, 2013)
> r2_m<-r.squaredGLMM(res_m)
The result is correct only if all data used by the model has not chang
ed since model was fitted.
> R2<-rbind(R2,r2_mfull1)
Error in rbind(R2, r2_mfull1) : object 'r2_mfull1' not found
>
>
> cat("\n\n\n\n Use of space only \n\n\n")

```

Use of space only

```

> #Run full the model
>
> res_iu=glmer(winner_analysis ~ rel_UD190+
+             (1|dyad), family="binomial", data=factors_original)
>
>
> print(summary(res_iu))
Generalized linear mixed model fit by maximum likelihood (Laplace Appr
oximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_UD190 + (1 | dyad)
Data: factors_original

            AIC          BIC    logLik deviance df.resid
      126.9       134.5     -60.4    120.9        91

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.27978 -0.93253  0.03093  0.79660  1.84940

Random effects:
Groups Name          Variance Std.Dev.
dyad (Intercept) 0.539      0.7342
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.210371   0.571357  -0.368   0.713
rel_UD190    0.013332   0.006069   2.197   0.028 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr)
rel_UD190 -0.049
>
>
> cat("\n\n\n Comparison of male based model (full1) to null model\n\n
")

```

```

Comparison of male based model (full1) to null model

> print(anova(res.null,res_iu, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_iu: winner_analysis ~ rel_UD190 + (1 | dyad)
      Df    AIC    BIC  logLik deviance Chisq Chi Df Pr(>Chisq)
res.null 2 130.19 135.27 -63.093   126.19      1  1 0.02106 *
res_iu   3 126.86 134.49 -60.432   120.86      1  1 0.02106 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> #The full model wasn't significant (but almost) so no adj. model is
produced
>
> #AIC values to the list
> models[[4]]<-res_iu
> Modnames <- rbind(Modnames, "I.U.")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and
Schielzeth, 2013)
> r2_iu<-r.squaredGLMM(res_iu)
The result is correct only if all data used by the model has not chang
ed since model was fitted.
> R2<-rbind(R2,r2_iu)
>
>
> #####
#####
> #####
#####
> #####
#####
> cat("\n\n RESULTS \n\n")

```

RESULTS

```

> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs
= NULL, sort = TRUE)

```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcwt	Cum.Wt	LL
I.U.	3	127.13	0.00	0.49	0.49	-60.43
Female based	4	128.67	1.54	0.22	0.71	-60.11
Male based	4	128.99	1.86	0.19	0.90	-60.27
null model	2	130.32	3.19	0.10	1.00	-63.09

Warning message:

```

In data.row.names(row.names, row si, i) :
some row.names duplicated: 3,4 --> row.names NOT used
> R2

```

	R2m	R2c
R2	0.00000000	0.09929656


```

r2_f  0.07859436 0.17636486
r2_iu 0.06951769 0.20050198

```

```

#####
##with interactions####

```

```

#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()

```

```

## Upload data
factors_original<-read.csv("factors_originalv1.csv")

```

```

#### Flip the variables for pb1-r1 so R1 is the focal group in all the encounters with decided outcome

```

```

#Checking the original data
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]

```

```

#Flipping pb1-r1 to r1-pb1
factors_original$winner_analysis[ factors_original$dyad=="pb1r1"] <-1-
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_groupsize[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_groupsize[
factors_original$dyad=="pb1r1"]
factors_original$rel_nummales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_nummales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numfemales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numfemales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numinfperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfperfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfpermale[
factors_original$dyad=="pb1r1"]
factors_original$rel_numswfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numswfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swgs[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swgs[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfemperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfemperfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfempermale[
factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_sexratio[
factors_original$dyad=="pb1r1"]
factors_original$rel_UD190[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_UD190[factors_original$dyad=="pb1r1"]
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"]

```

```

#Checking that the flipping worked
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]

####Convert variables to the appropriate format
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$winner_analysis<- as.numeric(factors_original$winner_analysis)#If written as factor at this
stage, the flipping goes wrong
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$rel_numfemales<- as.numeric(factors_original$rel_numfemales)
factors_original$rel_nummales<- as.numeric(factors_original$rel_nummales)
factors_original$rel_UD190<- as.numeric(factors_original$rel_UD190)
factors_original$winner_analysis<- as.factor(factors_original$winner_analysis)#Now we can transform it into
factor without problems

#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison
cannot be made)
missingrows = is.na(factors_original$rel_nummales)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numfemales)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numinfpermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numinfpermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_sexratio)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$winner_analysis)
factors_original= factors_original[!missingrows,]

```

The result is correct only if all data used by the model has not changed since model was fitted.

```

> R2<-r2_null
>
>
> cat("\n\n\ Checking potential control variables: Duration and number
of observers \n\n")

```

Checking potential control variables: Duration and number of observers

```

>
> res_cv=glmer(winner_analysis ~durationIGE+num_obs+(1|dyad), family="
binomial", data=factors_original)
>
> print(summary(res_cv))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

```

```

Family: binomial ( logit )
Formula: winner_analysis ~ durationIGE + num_obs + (1 | dyad)
Data: factors_original

      AIC      BIC    logLik deviance df.resid
  130.0    140.1    -61.0    122.0      90

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.84259 -0.85489  0.08184  0.85079  1.91944

Random effects:
 Groups Name      Variance Std.Dev.
 dyad    (Intercept) 0.1797   0.4239
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.696607   0.656073  -1.062   0.2883
durationIGE -0.003549   0.002153  -1.648   0.0993 .
num_obs      0.455778   0.279727   1.629   0.1032
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) drtIGE
durationIGE -0.028
num_obs     -0.741 -0.388
>
> #Comparison between the null model and the model with c.v
> print(anova(res.null,res_cv, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_cv: winner_analysis ~ durationIGE + num_obs + (1 | dyad)
      Df      AIC      BIC    logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 130.19 135.27 -63.093   126.19
res_cv    4 129.96 140.13 -60.979   121.96 4.2285    2    0.1207
>
>
>
>
> #Check that no combination between response and random effects is to
o unfrequent
> table(factors_original$winner_analysis, factors_original$dyad)

      pb1r1 pb1r2 r1r2
0         23      0   24
1         37      0   10
>
>
>
>
> cat("\n\n\n\n\n\n\n\n Female-based model with use of space \n\n\n\n\n\n\n\n\n")

```

Female-based model with use of space

```

>
> # Response: winner_analysis (binary, 1=Focal group wins, 0= Focal group loses)
> # Fixed effects: rel_numfemales+rel_numinfperfem+rel_swfemperfem+rel_sexratio+rel_UD190
> # Random effect: 'dyad', 2 levels.
> # Hypothesis: "A group would have increased odds of winning (1) when its number of females was larger than its opponent,
> # (2) when the proportion of infants/female is smaller (3) when the proportion of fertile females/female is smaller
> # (4) when the sex ratios (f:m) is higher than those of the opponent
>
> #Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
> vif(glm(winner_analysis ~ rel_numfemales+rel_UD190, family="binomial", data=factors_original))
      rel_numfemales      rel_UD190
      1.077043      1.077043
>
> #Run the model
> res_f=glmer(winner_analysis ~
+             rel_numfemales+rel_UD190+rel_numfemales*rel_UD190+
+             (1|dyad), family="binomial", data=factors_original)
Warning messages:
1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv,
:      Model failed to converge with max|grad| = 0.00247261 (tol = 0.001, component 1)
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv,
:      Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?; Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
>
> print(summary(res_f))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_numfemales + rel_UD190 + rel_numfemales * rel_UD190 + (1 | dyad)
Data: factors_original

      AIC      BIC    logLik deviance df.resid
  127.3   140.0   -58.6    117.3      89

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.39892 -0.75470 -0.07266  0.77877  1.88362

Random effects:
Groups Name      Variance Std.Dev.
dyad (Intercept) 0.4784    0.6917
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -1.109159   1.492644  -0.743   0.4574
rel_numfemales    0.128976   0.185050   0.697   0.4858
rel_UD190       -0.039195   0.031134  -1.259   0.2081
rel_numfemales:rel_UD190  0.007256   0.004289   1.692   0.0907 .
---

```

```

Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) r1_nmf r_UD19
rel_numfmls  -0.930
rel_UD190    -0.062  0.035
r1_n:_UD190   0.035 -0.008 -0.981
convergence code: 0
Model failed to converge with max|grad| = 0.00247261 (tol = 0.001, com
ponent 1)
Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?
Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?

>
> cat("\n\n\n Comparison of female-based (full; UD) model to null mode
l\n\n")

Comparison of female-based (full; UD) model to null model

>
> print(anova(res.null,res_f, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_f: winner_analysis ~ rel_numfemales + rel_UD190 + rel_numfemales *
res_f:      rel_UD190 + (1 | dyad)
      Df      AIC      BIC    logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 130.19 135.27 -63.093    126.19
res_f     5 127.28 140.00 -58.641    117.28 8.9041      3    0.03059 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> #AIC values to the list
> models[[2]]<-res_f
> Modnames <- rbind(Modnames, "Female based")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and
Schielzeth, 2013)
> r2_f<-r.squaredGLMM(res_f)
The result is correct only if all data used by the model has not chang
ed since model was fitted.
Warning messages:
1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv
, : Model failed to converge with max|grad| = 0.0023714 (tol = 0.001, co
mponent 1)
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv
, : Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?;Model is nearly unidentifiable: large eigenvalue
ratio
- Rescale variables?
> R2<-rbind(R2,r2_f)
>
>
>
> cat("\n\n\n\n\n\n\n\n Male-based model with UD_190\n\n\n\n\n\n\n\n\n
")

```

Male-based model with UD_190

```
>
>
>
> cat("\n\n\n\n Male-based model 1 \n\n\n")
```

Male-based model 1

```
> #Run full the model
>
> res_m=glmer(winner_analysis ~ rel_nummales+rel_UD190+rel_nummales*rel_UD190+
+             (1|dyad), family="binomial", data=factors_original)
Warning messages:
1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv
, : Model failed to converge with max|grad| = 0.0108248 (tol = 0.001, component 1)
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv
, : Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?;Model is nearly unidentifiable: large eigenvalue
ratio
- Rescale variables?
>
>
> print(summary(res_m))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_nummales + rel_UD190 + rel_nummales * rel_UD190 + (1 | dyad)
Data: factors_original

            AIC      BIC    logLik deviance df.resid
      128.7      141.4     -59.3    118.7        89

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.52461 -0.77094  0.03914  0.79194  1.89735

Random effects:
Groups Name      Variance Std.Dev.
dyad (Intercept) 0.8153   0.903
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.723649   2.734040   0.630    0.528
rel_nummales   -0.299806   0.421741  -0.711    0.477
rel_UD190      -0.055931   0.052519  -1.065    0.287
rel_nummales:rel_UD190 0.010801   0.008173   1.321    0.186
```

```

Correlation of Fixed Effects:
              (Intr) rl_nmm r_UD19
rel_nummals  -0.968
rel_UD190    -0.106  0.096
rl_n:_UD190  0.109 -0.100 -0.993
convergence code: 0
Model failed to converge with max|grad| = 0.0108248 (tol = 0.001, comp
onent 1)
Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?
Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?

>
>
") > cat("\n\n\n Comparison of male based model (full1) to null model\n\n

Comparison of male based model (full1) to null model

> print(anova(res.null,res_m, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_m: winner_analysis ~ rel_nummales + rel_UD190 + rel_nummales * rel
_UD190 +
res_m:      (1 | dyad)
              Df      AIC      BIC    logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null    2 130.19 135.27 -63.093   126.19
res_m       5 128.69 141.41 -59.346   118.69 7.4949      3   0.05769 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> #The full model wasn't significant (but almost) so no adj. model is
produced
>
> #AIC values to the list
> models[[3]]<-res_m
> Modnames <- rbind(Modnames, "Male based")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and
Schielzeth, 2013)
> r2_m<-r.squaredGLMM(res_m)
The result is correct only if all data used by the model has not chang
ed since model was fitted.
warning messages:
1: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv
, :
Model failed to converge with max|grad| = 0.0031208 (tol = 0.001, co
mponent 1)
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv
, :
Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?;Model is nearly unidentifiable: large eigenvalue
ratio
- Rescale variables?
> R2<-rbind(R2,r2_m)
>
>
> cat("\n\n\n\n Use of space only \n\n\n")

```

Use of space only

```

> #Run full the model
>
> res_iu=glmer(winner_analysis ~ rel_UD190+
+             (1|dyad), family="binomial", data=factors_original)
>
>
> print(summary(res_iu))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_UD190 + (1 | dyad)
Data: factors_original

            AIC      BIC    logLik deviance df.resid
      126.9      134.5     -60.4    120.9        91

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.27978 -0.93253  0.03093  0.79660  1.84940

Random effects:
Groups Name      Variance Std.Dev.
dyad (Intercept) 0.539     0.7342
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.210371    0.571357  -0.368   0.713
rel_UD190    0.013332    0.006069   2.197   0.028 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr)
rel_UD190 -0.049
>
>
> cat("\n\n Comparison of male based model (full1) to null model\n\n
")

      Comparison of male based model (full1) to null model

> print(anova(res.null,res_iu, test="Chisq"))
Data: factors_original
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_iu: winner_analysis ~ rel_UD190 + (1 | dyad)
      Df      AIC      BIC    logLik deviance Chisq Chi Df Pr(>Chisq)
res.null  2 130.19 135.27 -63.093    126.19
res_iu    3 126.86 134.49 -60.432    120.86 5.322      1    0.02106 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
> #The full model wasn't significant (but almost) so no adj. model is
produced
>
> #AIC values to the list
> models[[4]]<-res_iu
> Modnames <- rbind(Modnames, "I.U.")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and
Schielzeth, 2013)
> r2_iu<-r.squaredGLMM(res_iu)
The result is correct only if all data used by the model has not chang
ed since model was fitted.
> R2<-rbind(R2,r2_iu)
>

```



```

>
> #####
#####
> #####
#####
> #####
#####
> cat("\n\n RESULTS \n\n")

```

RESULTS

```

> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs
= NULL, sort = TRUE)

```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcwt	Cum.Wt	LL
I.U.	3	127.13	0.00	0.46	0.46	-60.43
Female based	5	127.96	0.83	0.30	0.76	-58.64
Male based	5	129.37	2.24	0.15	0.91	-59.35
null model	2	130.32	3.19	0.09	1.00	-63.09

Warning message:

```

In data.row.names(row.names, rowsi, i) :
  some row.names duplicated: 3,4 --> row.names NOT used

```

```

> R2

```

	R2	R2m	R2c
R2	0.00000000	0.09929656	
r2_f	0.11877126	0.23065689	
r2_m	0.10725512	0.28456887	
r2_iu	0.06951769	0.20050198	

3.3. Replacing ratio variables for interger variables in the models of chapter 3

What follows a series of analyses comparing models performed with the variables used in the thesis in the form of ratios (e.g. No.infats per females) and models performed used integer variables (e.g. No. infants). Note that sex ratio has been omitted in the following models since there is no replacement of it in an interger version. Therefore, the results are different from those presented in the thesis itself.

```

## download packages

```

```

install.packages("lme4")#Package that allows to calculate the glms

```

```

install.packages("car")#Package to check regression "quality"

```

```

install.packages("ggplot2")# To plot independent variables and glms

```

```

install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone
account for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("ppcor")#To check for correlations between independent variables
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle
2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine

library(lme4)
library(car)
library(ggplot2)
library(modEvA)
library(languageR)
library(ppcor)
library(AICcmodavg)
library(MuMIn)
library(dplyr)
library(sjPlot)

> #Set directory
> setwd("C:/Users/Laura/Dropbox/PhD/THESIS/_PostViva_Revision/Revision_Ch3")
> getwd()
[1] "C:/Users/Laura/Dropbox/PhD/THESIS/_PostViva_Revision/Revision_Ch3"
>
>
>
> ## Upload data
> data<-read.csv("Data_for_revision_subsample.csv")
> ##### Flip the variables for pb1-r1 so R1 is the focal group in all the e
ncounters with decided outcome
>
> #Checking the original data
> data$winner_analysis[data$dyad=="pb1r1"]
[1] 0 1 0 1 NA 0 0 1 0 0 0 1 0 0 1 0 0 0 0 0 0 1 NA
0 1 0 1 NA NA 1 1 1 0 1 1 0 0 1 0 0 1 0 0 NA 0 NA NA NA
1 0 0 NA 1 1 0 NA 0 0 1 0 0 NA
[63] NA 0 0 NA 0 0 0
> data$rel_numfemales[data$dyad=="pb1r1"]
[1] -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9 -9
-9 -9 -9 -9 -9 -9 -9 -9 -8 -9 -9 -8 -8 -8 -8 -8 -8 -8 -8 -8 -8 -8 -8 -8
-8 -8 -8 -8 -8 -8 -8 -8 -8 -7 -7 -7 -3 -3
[63] -3 -7 -7 -7 -6 -6 -8
> data$rel_numinfperfem[data$dyad=="pb1r1"]
[1] -0.101724138 -0.101724138 -0.101724138 -0.101724138 -0.101724138 -0.1
01724138 -0.101724138 -0.101724138 0.101724138 0.101724138 0.101724138
0.101724138 0.101724138 0.101724138
[15] 0.101724138 0.001724138 0.086206897 0.120689655 0.220689655 0.2
20689655 0.220689655 0.220689655 0.151724138 0.151724138 0.151724138
0.151724138 0.151724138 0.251724138
[29] 0.251724138 0.251724138 0.251724138 0.235714286 0.251724138 0.2
51724138 0.218390805 0.218390805 0.218390805 0.218390805 0.218390805
0.218390805 0.218390805 0.218390805
[43] 0.218390805 0.266009852 0.266009852 0.266009852 0.266009852 0.2
66009852 0.266009852 0.266009852 0.266009852 0.266009852 0.266009852
0.266009852 0.266009852 0.266009852

```

```

[57] 0.300492611 0.347962382 0.347962382 0.347962382 0.287272727 0.2
87272727 0.287272727 0.347962382 0.347962382 0.382445141 0.461038961
0.461038961 0.451515152
>
> #Flipping pb1-r1 to r1-pb1
> data$winner_analysis[ data$dyad=="pb1r1"] <-1-data$winner_analysis[data$
dyad=="pb1r1"]
> data$rel_numfemales[ data$dyad=="pb1r1"] <- -data$rel_numfemales[ data$d
yad=="pb1r1"]
> data$rel_infants[ data$dyad=="pb1r1"] <- -data$rel_infants[ data$dyad=="
pb1r1"]
> data$rel_numinfperfem[ data$dyad=="pb1r1"] <- -data$rel_numinfperfem[ da
ta$dyad=="pb1r1"]
> data$rel_numswfem[ data$dyad=="pb1r1"] <- -data$rel_numswfem[ data$dyad=
=="pb1r1"]
> data$rel_swfemperfem[ data$dyad=="pb1r1"] <- -data$rel_swfemperfem[ data
$dyad=="pb1r1"]
> data$rel_UD190[data$dyad=="pb1r1"] <- -data$rel_UD190[data$dyad=="pb1r1"
]
>
>
>
> #Checking that the flipping worked
> data$winner_analysis[data$dyad=="pb1r1"]
[1] 1 0 1 0 NA 1 1 0 1 1 1 0 1 1 0 1 1 1 1 1 0 NA
1 0 1 0 NA NA 0 0 0 1 0 0 1 1 0 1 1 0 1 1 NA 1 NA NA NA
0 1 1 NA 0 0 1 NA 1 1 0 1 1 NA
[63] NA 1 1 NA 1 1 1
> data$rel_numfemales[data$dyad=="pb1r1"]
[1] 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 8 9 9 8
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 7 7 7 3 3 3 7 7 7 6 6 8
> data$rel_numinfperfem[data$dyad=="pb1r1"]
[1] 0.101724138 0.101724138 0.101724138 0.101724138 0.101724138 0.1
01724138 0.101724138 0.101724138 -0.101724138 -0.101724138 -0.101724138
-0.101724138 -0.101724138 -0.101724138
[15] -0.101724138 -0.001724138 -0.086206897 -0.120689655 -0.220689655 -0.2
20689655 -0.220689655 -0.220689655 -0.151724138 -0.151724138 -0.151724138
-0.151724138 -0.151724138 -0.251724138
[29] -0.251724138 -0.251724138 -0.251724138 -0.235714286 -0.251724138 -0.2
51724138 -0.218390805 -0.218390805 -0.218390805 -0.218390805 -0.218390805
-0.218390805 -0.218390805 -0.218390805
[43] -0.218390805 -0.266009852 -0.266009852 -0.266009852 -0.266009852 -0.2
66009852 -0.266009852 -0.266009852 -0.266009852 -0.266009852 -0.266009852
-0.266009852 -0.266009852 -0.266009852
[57] -0.300492611 -0.347962382 -0.347962382 -0.347962382 -0.287272727 -0.2
87272727 -0.287272727 -0.347962382 -0.347962382 -0.382445141 -0.461038961
-0.461038961 -0.451515152
>
>
> ###Convert variables to the appropriate format
> data$num_obs<- as.numeric(data$num_obs)
> data$dyad<- factor(data$dyad)
> data$winner_analysis<- as.numeric(data$winner_analysis)#If writen as fac
tor at this stage, the flipping goes wrong
> data$durationIGE<- as.numeric(data$durationIGE)
> data$rel_numfemales<- as.numeric(data$rel_numfemales)
> data$rel_infants<- as.numeric(data$rel_infants)
> data$rel_numinfperfem<- as.numeric(data$rel_numinfperfem)
> data$rel_numswfem<- as.numeric(data$rel_numswfem)
> data$rel_swfemperfem<- as.numeric(data$rel_swfemperfem)

```

```
> data$rel_UD190<- as.numeric(data$rel_UD190)
> data$winner_analysis<- as.factor(data$winner_analysis)#Now we can transform it into factor without problems
>
> #Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison cannot be made)
> missingrows = is.na(data$rel_numfemales)
> data= data[!missingrows,]
> missingrows = is.na(data$rel_numinfperfem)
> data= data[!missingrows,]
> missingrows = is.na(data$rel_swfemperfem)
> data= data[!missingrows,]
> missingrows = is.na(data$winner_analysis)
> data= data[!missingrows,]
```

```
> cat("\n\n\n Checking correlations between fixed effects in each set of variables \n\n\n")
```

Checking correlations between fixed effects in each set of variables

```
>
> #Correlations between variables used in the original models (rel_numfemales, rel_numinfperfem and rel_swfemperfem and rel_UD190)
> dataf_original<-data.frame(data$rel_numfemales,data$rel_numinfperfem,data$rel_swfemperfem,data$rel_UD190)
> pcor(dataf_original)
```

\$estimate	data.rel_numfemales	data.rel_numinfperfem	data.rel_swfemperfem	data.rel_UD190
data.rel_numfemales	1.00000000	0.1930695	-0.02512023	-0.08290612
data.rel_numinfperfem	0.19306949	1.00000000	-0.30679637	-0.1227689
data.rel_swfemperfem	-0.02512023	-0.3067964	1.00000000	0.02530666
data.rel_UD190	-0.08290612	-0.1227689	0.02530666	1.00000000

\$p.value	data.rel_numfemales	data.rel_numinfperfem	data.rel_swfemperfem	data.rel_UD190
data.rel_numfemales	0.0000000	0.074904105	0.818415941	0.479141
data.rel_numinfperfem	0.0749041	0.000000000	0.004064507	0.601155
data.rel_swfemperfem	0.8184159	0.004064507	0.000000000	0.170917
data.rel_UD190	0.4479141	0.260115550	0.817091670	0.000000

\$statistic	data.rel_numfemales	data.rel_numinfperfem	data.rel_swfemperfem	data.rel_UD190
data.rel_numfemales	0.0000000	0.074904105	0.818415941	0.479141
data.rel_numinfperfem	0.0749041	0.000000000	0.004064507	0.601155
data.rel_swfemperfem	0.8184159	0.004064507	0.000000000	0.170917
data.rel_UD190	0.4479141	0.260115550	0.817091670	0.000000

```

data.rel_numfemales      0.0000000      1.803443      -0.2303034      -0.7
624721
data.rel_numinfperfem    1.8034428      0.000000      -2.9543061      -1.1
337721
data.rel_swfemperfem     -0.2303034      -2.954306      0.0000000      0.2
320137
data.rel_UD190           -0.7624721      -1.133772      0.2320137      0.0
000000

$n
[1] 88

$gp
[1] 2

$method
[1] "pearson"

>
>
> #Correlations between the new variables (rel_infants, rel_numswfem) and
those which don't change (rel_numfemales and rel_UD190)
> dataf_new<-data.frame(data$rel_numfemales,data$rel_infants, data$rel_num
swfem,data$rel_UD190)
> pcor(dataf_new)
$estimate
              data.rel_numfemales data.rel_infants data.rel_numswfem data.rel_UD190
data.rel_numfemales      1.0000000      0.4752448      0.11181199      -0.03163805
data.rel_infants         0.4752448      1.0000000      -0.29359344      -0.14235372
data.rel_numswfem        0.11181199      -0.2935934      1.00000000      0.01440587
data.rel_UD190           -0.03163805      -0.1423537      0.01440587      1.00000000

$p.value
              data.rel_numfemales data.rel_infants data.rel_numswfem data.rel_UD190
data.rel_numfemales      0.000000e+00      3.768628e-06      0.305388241      0.7724449
data.rel_infants         3.768628e-06      0.000000e+00      0.006077445      0.1910476
data.rel_numswfem        3.053882e-01      6.077445e-03      0.000000000      0.8952639
data.rel_UD190           7.724449e-01      1.910476e-01      0.895263931      0.0000000

$statistic
              data.rel_numfemales data.rel_infants data.rel_numswfem data.rel_UD190
data.rel_numfemales      0.0000000      4.950472      1.0312403      -0.2901128
data.rel_infants         4.9504723      0.000000      -2.8148789      -1.3181173
data.rel_numswfem        1.0312403      -2.814879      0.0000000      0.1320457
data.rel_UD190           -0.2901128      -1.318117      0.1320457      0.0000000

$n
[1] 88

$gp
[1] 2

$method
[1] "pearson"

>
> #More significant correlations between new than old variables
> cat("\n\n\n\n\n Null model \n\n\n\n\n")

```

Null model

```
>
>
> res.null=glmer(winner_analysis ~ 1+ (1|dyad), family="binomial", data=data)
>
> #AIC values to the list
> models<-list()
> models[[1]]<-res.null
> Modnames <- "null model"
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_null<-r.squaredGLMM(res.null)
The result is correct only if all data used by the model has not changed since model was fitted.
> R2<-r2_null
> cat("\n\n\n\n\n\n\n\n Using original variables (Proportions of tumescent females and infants per female) \n\n\n\n\n\n\n\n\n\n")
```

Using original variables (Proportions of tumescent females and infants per female)

```
>
>
> #Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
> vif(glm(winner_analysis ~ rel_numfemales+rel_numinfperfem+rel_swfemperfem+rel_UD190, family="binomial", data=data))
      rel_numfemales rel_numinfperfem rel_swfemperfem      rel_UD190
      1.101122      1.218187      1.171847      1.062169
>
> #Run the model
> res_original=glmer(winner_analysis ~
+ rel_numfemales+rel_numinfperfem+rel_swfemperfem+rel_UD190+
+ (1|dyad), family="binomial", data=data)
>
```

```

> print(summary(res_original))
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_numfemales + rel_numinfperfem + rel_swfempe
rfem + rel_UD190 + (1 | dyad)
Data: data

      AIC      BIC    logLik deviance df.resid
    119.6    134.5    -53.8    107.6      82

Scaled residuals:
    Min      1Q   Median      3Q      Max
-1.5552 -0.9286  0.3892  0.7418  2.0323

Random effects:
Groups Name      Variance Std.Dev.
dyad   (Intercept) 0.4034   0.6351
Number of obs: 88, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.113478   1.800949  -0.618   0.5364
rel_numfemales  0.172254   0.204295   0.843   0.3991
rel_numinfperfem -1.790993   2.375574  -0.754   0.4509
rel_swfemperfem -4.074969   2.817384  -1.446   0.1481
rel_UD190      0.016674   0.006968   2.393   0.0167 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) r1_nmf r1_nmn r1_swf
rel_numfmls  -0.934
r1_nmnfprfm   0.475 -0.390
r1_swfmpfrfm -0.075 -0.061  0.313
rel_UD190     0.011  0.033  0.091 -0.153
>
> cat("\n\n Comparison of female-based (full; UD) model to null model\n\
n")

  comparison of female-based (full; UD) model to null model

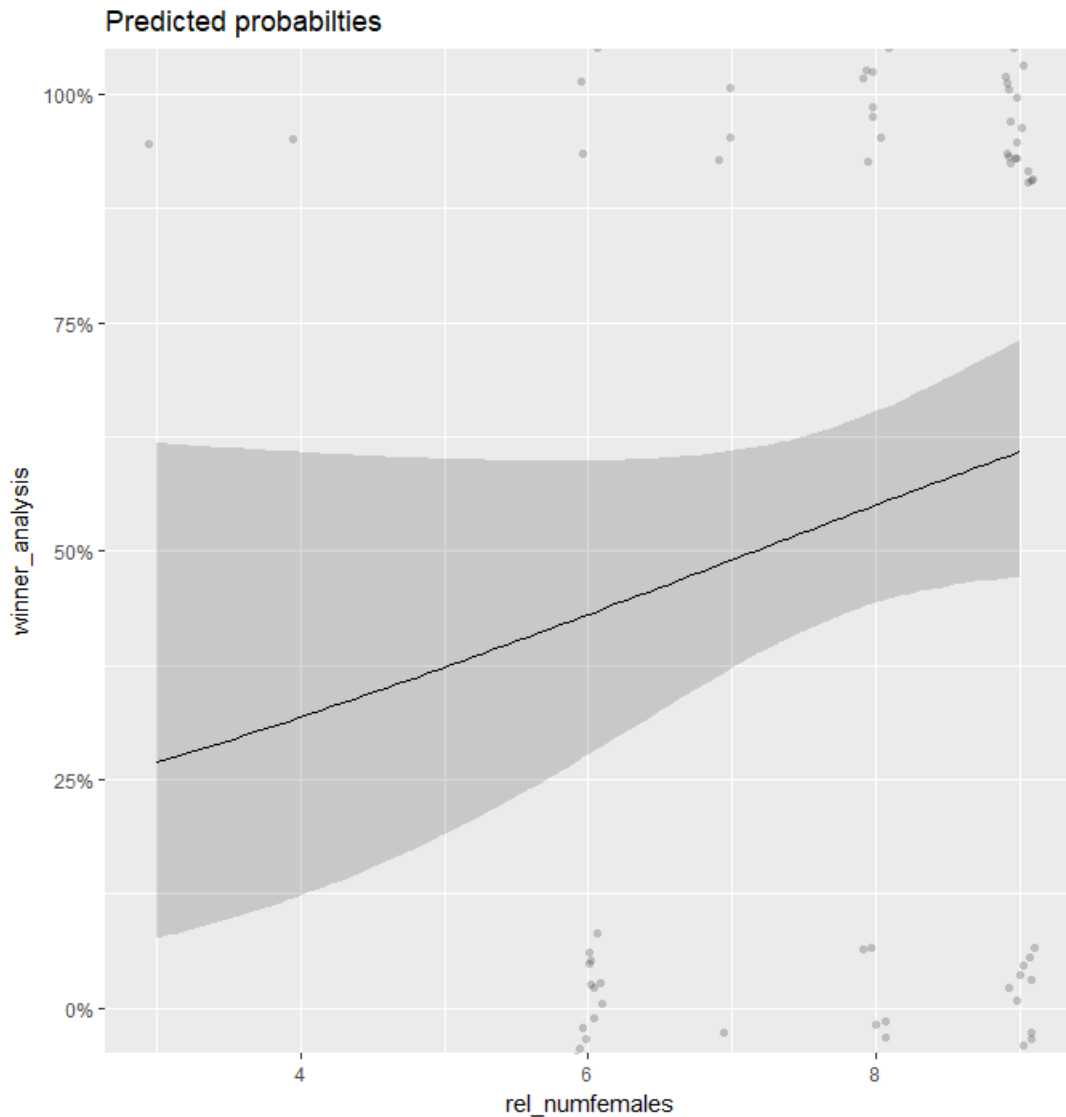
>
> print(anova(res.null,res_original, test="Chisq"))
Data: data
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_original: winner_analysis ~ rel_numfemales + rel_numinfperfem + rel_sw
femperfem +
res_original: rel_UD190 + (1 | dyad)
      Df      AIC      BIC    logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null    2 120.76 125.71 -58.378    116.76
res_original  6 119.60 134.46 -53.798    107.60  9.1593     4    0.05724 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> #AIC values to the list
> models[[2]]<-res_original

```

```

> Modnames <- rbind(Modnames, "Model with original variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_original<-r.squaredGLMM(res_original)
The result is correct only if all data used by the model has not changed since model was fitted.
> R2<-rbind(R2,r2_original)
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="rel_numfemales",geom.colors = "bw",show.ci=TRUE)

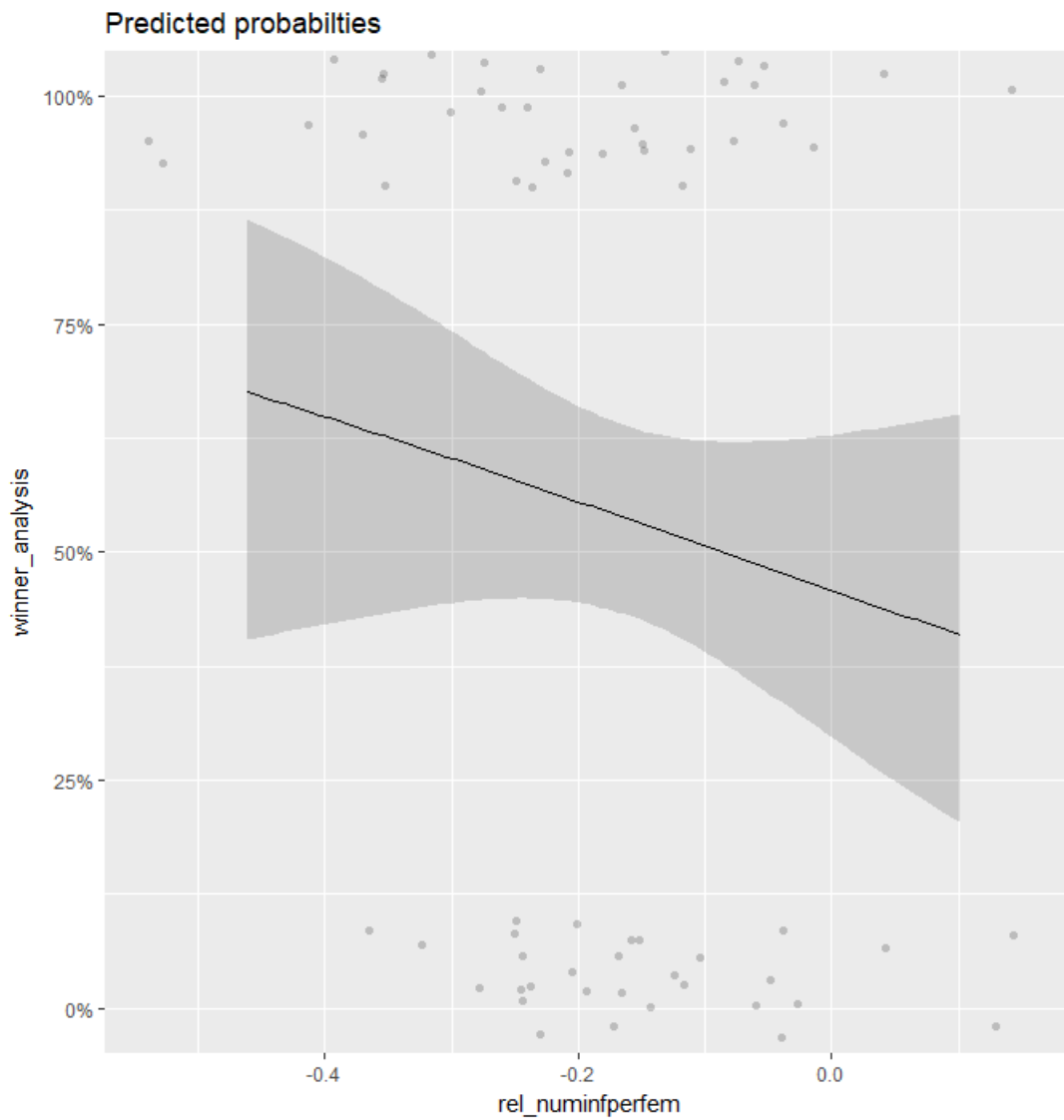
```



```

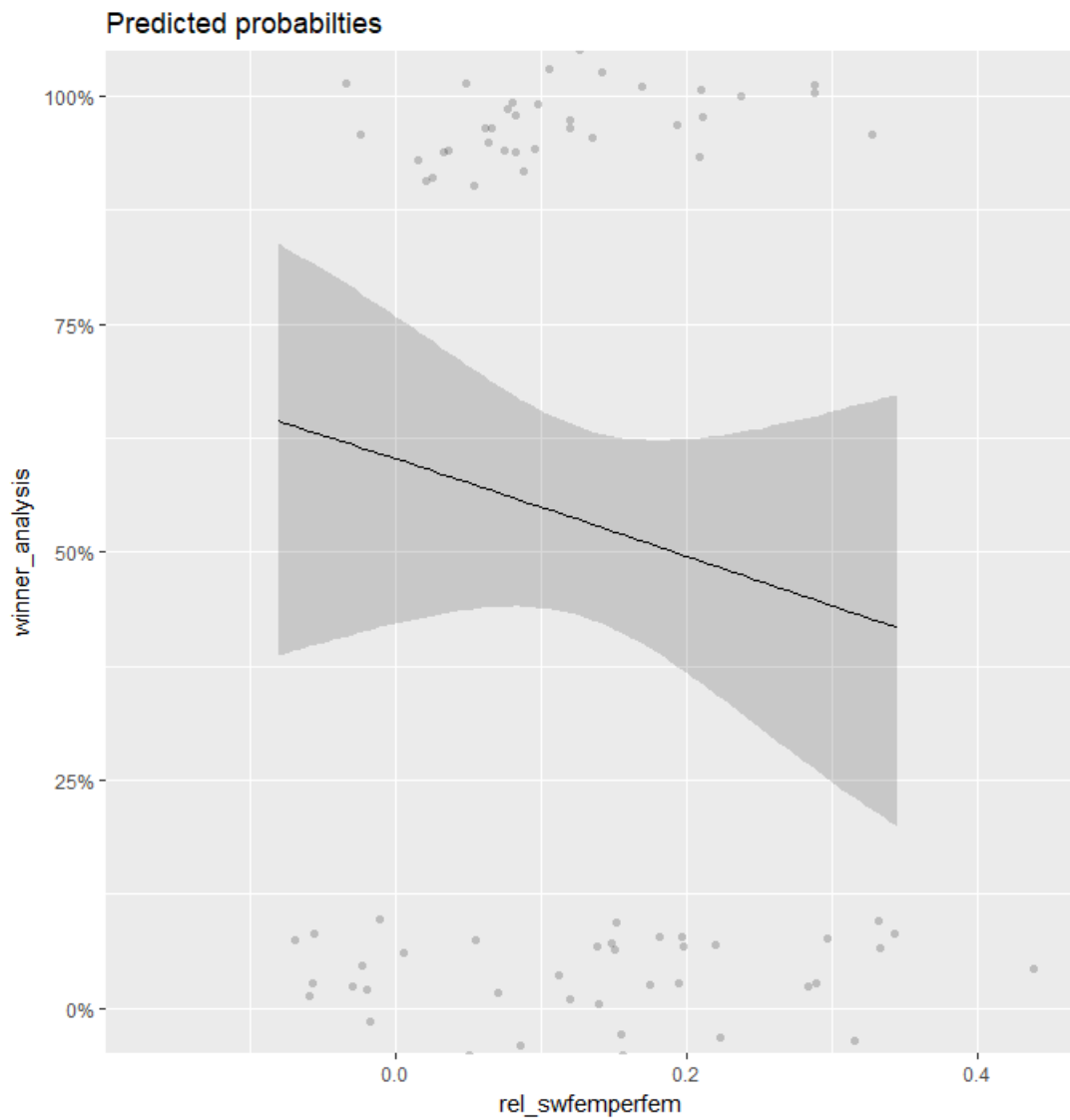
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="rel_numinfperferem",geom.colors = "bw",show.ci=TRUE)

```

```
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="rel_swfempe  
rfem",geom.colors = "bw",show.ci=TRUE)
```

``sjp.glmer()`` will become deprecated in the future. Please use ``plot_model
()`` instead.



```
> cat("\n\n\n\n\n\n\n\n Variables proposed in viva (No.infants/Females with infants and No. tumescent females) \n\n\n\n\n\n\n\n\n")
```

Variables proposed in viva (No.infants/Females with infants and No. tumescent females)

```
>
```

```

> #Checking co-linearity (Values close to 1 are good, over 4 can be problem)
> vif(glm(winner_analysis ~ rel_numfemales+rel_infants+rel_numswfem+rel_UD190, family="binomial", data=data))
rel_numfemales    rel_infants    rel_numswfem    rel_UD190
      1.395542      1.486303      1.160591      1.064515
>
> #Run the model
> res_new=glmer(winner_analysis ~
+               rel_numfemales+rel_infants+rel_numswfem+rel_UD190+
+               (1|dyad), family="binomial", data=data)
>
> print(summary(res_new))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_numfemales + rel_infants + rel_numswfem + rel_UD190 + (1 | dyad)
Data: data

            AIC      BIC    logLik deviance df.resid
      119.2    134.0    -53.6    107.2      82

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.6031 -0.9511  0.3820  0.7480  2.1266

Random effects:
Groups Name      Variance Std.Dev.
dyad    (Intercept) 0.3934   0.6272
Number of obs: 88, groups: dyad, 2

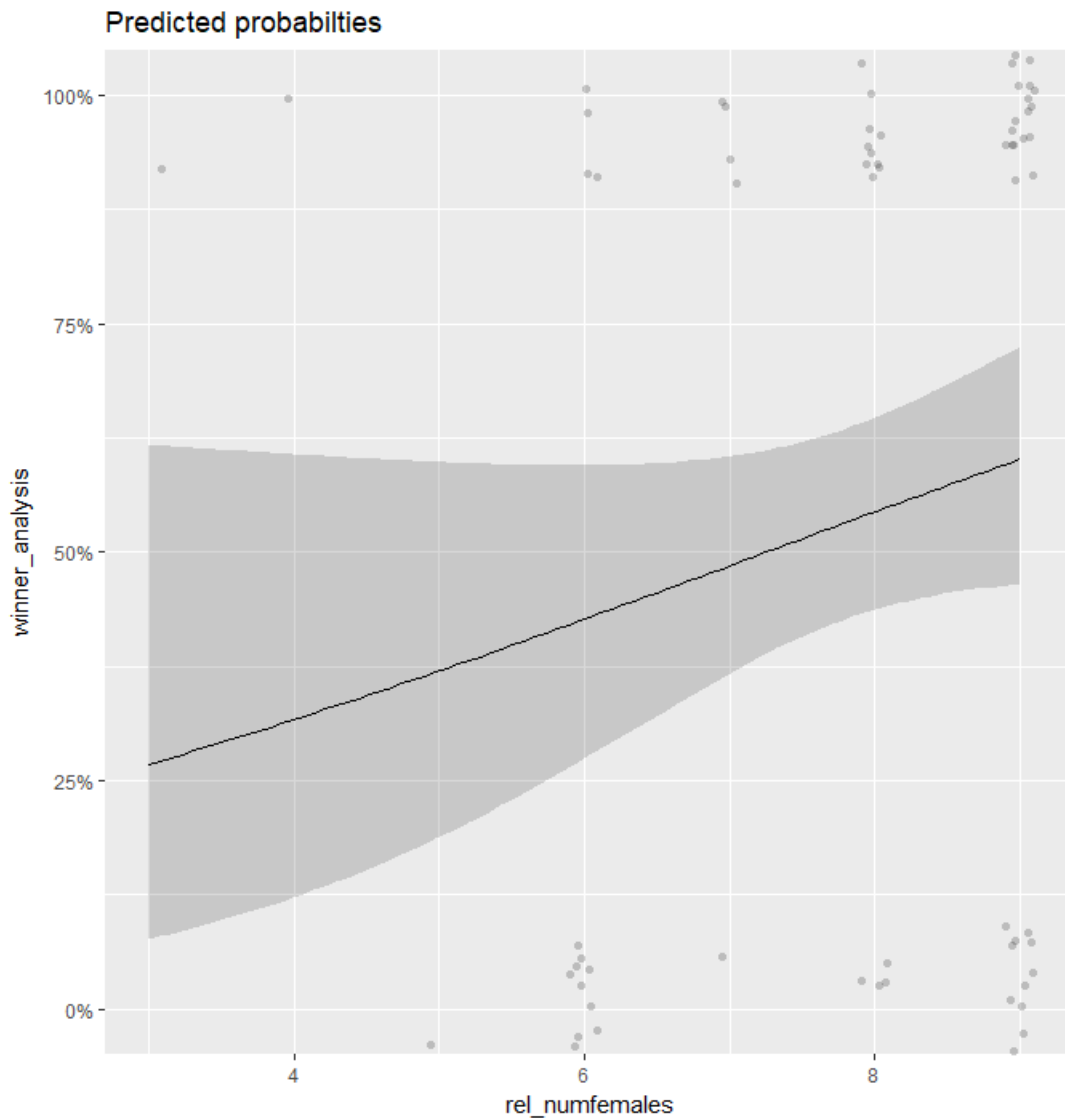
Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.251383   1.854610  -0.675   0.4998
rel_numfemales  0.246009   0.238499   1.031   0.3023
rel_infants    -0.083563   0.101775  -0.821   0.4116
rel_numswfem   -0.160137   0.102549  -1.562   0.1184
rel_UD190      0.016517   0.007009   2.356   0.0185 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) rl_nmf rl_nfn rl_nms
rel_numfmls  -0.937
rel_infants   0.525 -0.616
rel_numswfm  -0.054 -0.170  0.289
rel_UD190     0.028 -0.005  0.124 -0.144

> #AIC values to the list
> models[[3]]<-res_new
> Modnames <- rbind(Modnames, "Model with new variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_new<-r.squaredGLMM(res_new)
The result is correct only if all data used by the model has not changed since model was fitted.
> R2<-rbind(R2,r2_new)

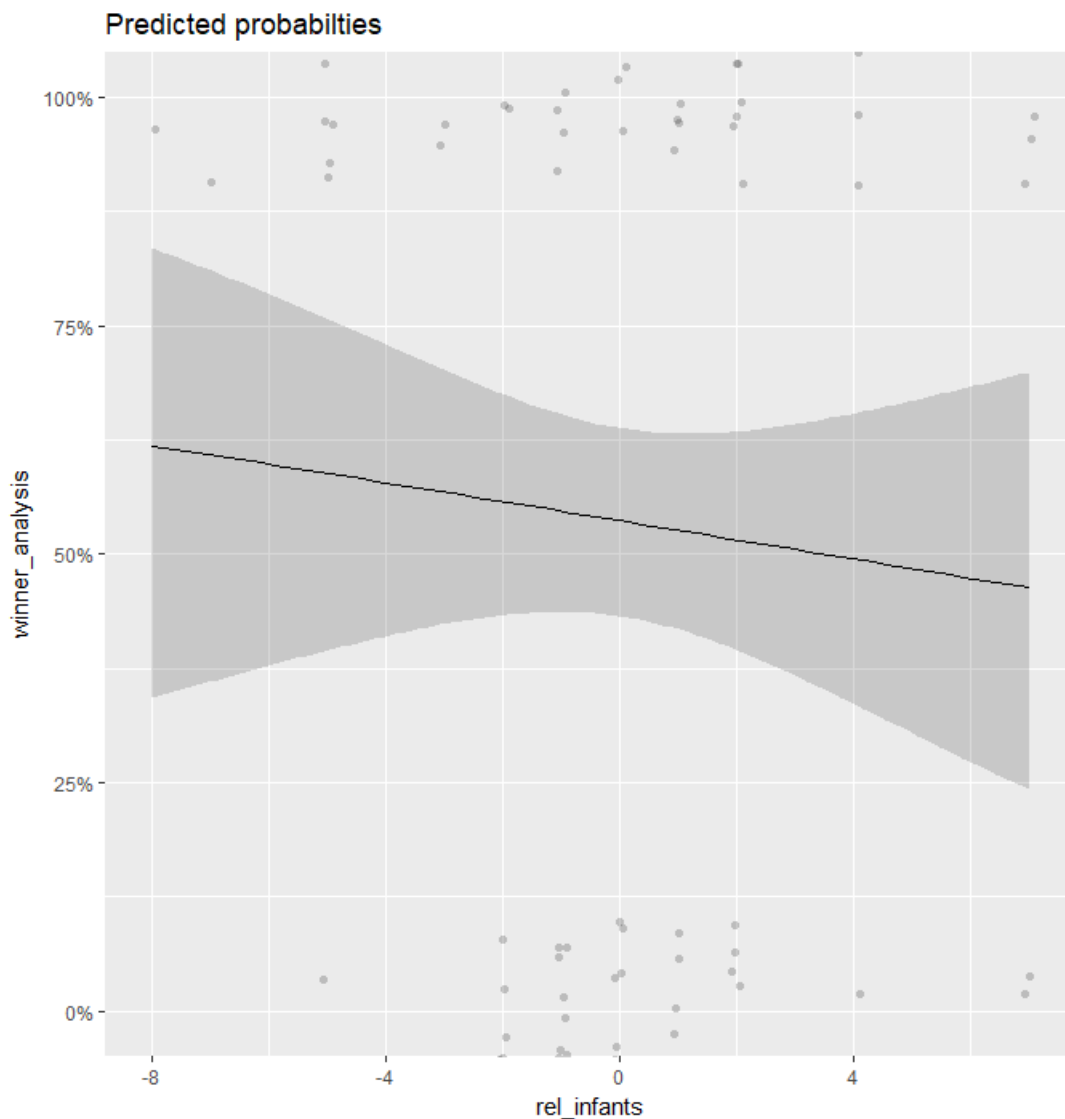
```

```
>
>
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="rel_numfemales",
geom.colors = "bw",show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model`
()` instead.
```

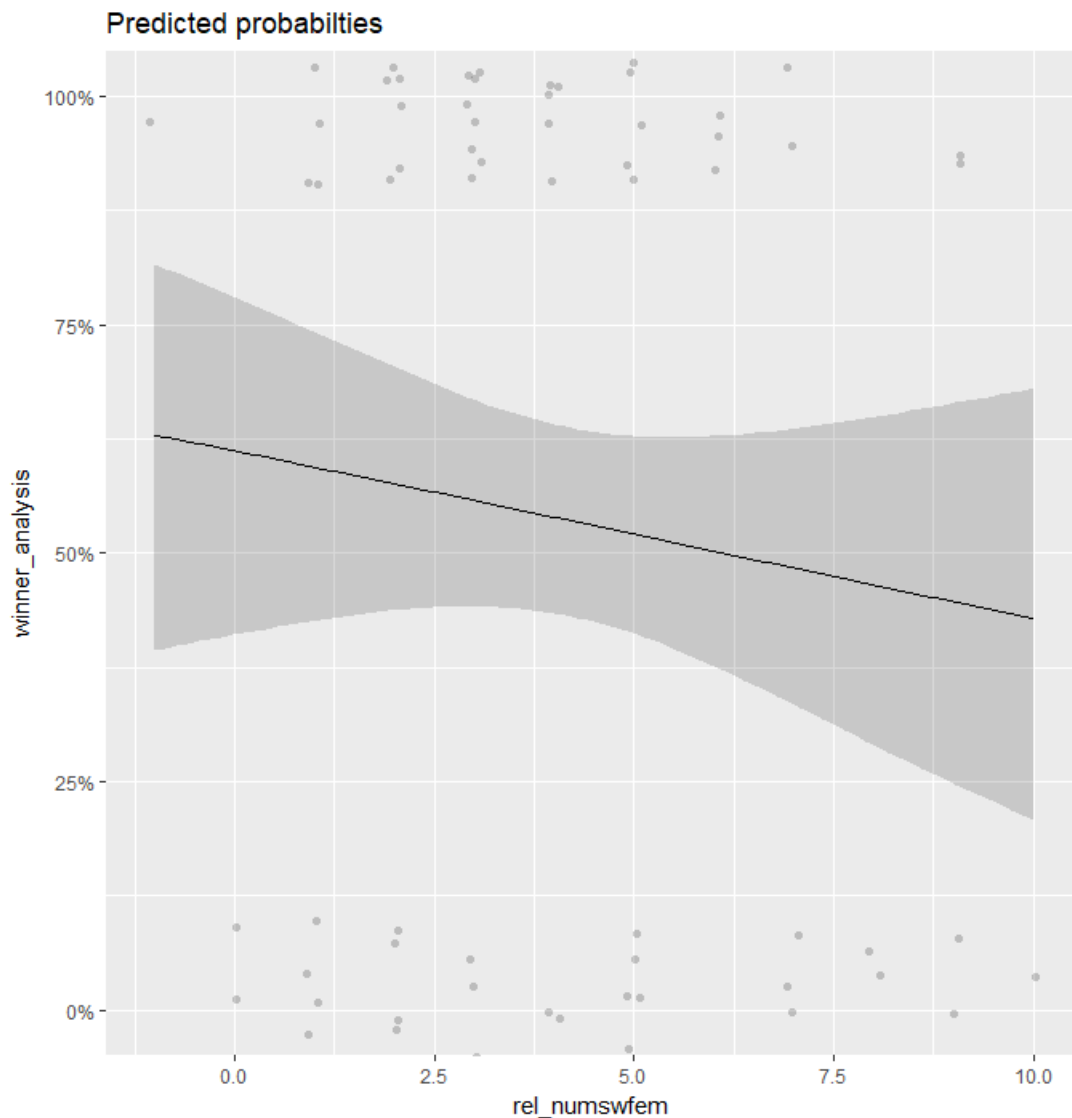


```
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="rel_infants",geo
m.colors = "bw",show.ci=TRUE)
```

``sjp.glmer()`` will become deprecated in the future. Please use ``plot_model()`` instead.



```
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="rel_numswfem", geom.colors = "bw", show.ci=TRUE)
```



```
>
> #####
> cat("\n\n\n RESULTS \n\n\n")
```

RESULTS

```
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = N
ULL, sort = TRUE)
```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcwt	Cum.Wt	LL
Model with new variables	6	120.20	0.00	0.40	0.40	-53.58
Model with original variables	6	120.63	0.44	0.32	0.72	-53.80
null model	2	120.90	0.70	0.28	1.00	-58.38

Warning message:
In data.row.names(row.names, rowsi, i) :

```

some row.names duplicated: 3 --> row.names NOT used
> R2
      R2m      R2c
R2      0.0000000 0.1162905
r2_original 0.1393451 0.2333535
r2_new     0.1460438 0.2372488

```

Female-based models with integer and ratio variables are equivalent in the trends shown, AICc and R^2 when using relative values

```

> cat("\n\n\n\n\n\n\n WHAT IF WE CHECK THE MALE-BASED MODELS INSTEAD? IS I
T STILL SIMILAR?\n\n\n\n\n\n")

```

WHAT IF WE CHECK THE MALE-BASED MODELS INSTEAD? IS IT STILL SIMILAR?

```

>
>
>
> cat("\n\nUsing original variables (Proportions of tumescent females and
infants per male) \n\n\n")
Error: '\U' used without hex digits in character string starting ""\n\n\U"
>
>
> #Checking co-linearity (values close to 1 are good, over 4 can be proble
matic)
> vif(glm(winner_analysis ~ rel_nummales+rel_numinfpermale+rel_swfempermale
+rel_UD190, family="binomial", data=data))
      rel_nummales rel_numinfpermale rel_swfempermale      rel_UD190
      7.297806      8.106746      1.707665      1.095050
> vif(glm(winner_analysis ~ rel_numinfpermale+rel_swfempermale+rel_UD190,
family="binomial", data=data))
rel_numinfpermale rel_swfempermale      rel_UD190
      1.792978      1.702956      1.086043
> vif(glm(winner_analysis ~ rel_nummales+rel_swfempermale+rel_UD190, fami
ly="binomial", data=data))
      rel_nummales rel_swfempermale      rel_UD190
      1.611179      1.525383      1.095431
>
> #Run the model
> res_ori_m1=glmer(winner_analysis ~
+ rel_numinfpermale+rel_swfempermale+rel_UD190+

```

```

+           (1|dyad), family="binomial", data=data)
>
> print(summary(res_ori_m1))
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_numinfpermale + rel_swfempermale + rel_UD19
0 + (1 | dyad)
Data: data

      AIC      BIC    logLik deviance df.resid
    112.9    125.3    -51.5    102.9      83

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.8804 -0.8605  0.3496  0.7701  2.1198

Random effects:
Groups Name      Variance Std.Dev.
dyad   (Intercept) 0         0
Number of obs: 88, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -0.268432   0.269694  -0.995   0.31958
rel_numinfpermale  0.552406   0.187523   2.946   0.00322 **
rel_swfempermale  0.418010   0.798099   0.524   0.60045
rel_UD190       0.016448   0.006862   2.397   0.01653 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) r1_nmn r1_swf
r1_nmnfprml  -0.455
r1_swfmprml  -0.209  0.628
rel_UD190    -0.060  0.224  0.008
>
> res_ori_m2=glmer(winner_analysis ~
+                 rel_nummales+rel_swfempermale+rel_UD190+
+                 (1|dyad), family="binomial", data=data)
>
> print(summary(res_ori_m2))
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_nummales + rel_swfempermale + rel_UD190 +
(1 | dyad)
Data: data

      AIC      BIC    logLik deviance df.resid
    114.2    126.6    -52.1    104.2      83

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.5429 -0.8913  0.3833  0.7386  1.9635

Random effects:
Groups Name      Variance Std.Dev.
dyad   (Intercept) 0         0
Number of obs: 88, groups: dyad, 2

```


Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-0.150902	0.256273	-0.589	0.55597
rel_nummales	-0.140900	0.050027	-2.816	0.00486 **
rel_swfempermale	0.111312	0.761054	0.146	0.88372
rel_UD190	0.016808	0.006812	2.467	0.01361 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	rl_nmm	rl_swf
rel_nummales	0.359		
rl_swfemprml	-0.098	-0.566	
rel_UD190	-0.052	-0.232	-0.020

>

> cat("\n\n Comparison of male-based models to null model\n\n")

Comparison of male-based models to null model

>

> print(anova(res.null,res_ori_m1, test="Chisq"))

Data: data

Models:

res.null: winner_analysis ~ 1 + (1 | dyad)

res_ori_m1: winner_analysis ~ rel_numinfpermale + rel_swfempermale + rel_UD190 +

res_ori_m1: (1 | dyad)

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
res.null	2	120.76	125.71	-58.378	116.76				
res_ori_m1	5	112.93	125.32	-51.467	102.93	13.823		3	0.003157 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> print(anova(res.null,res_ori_m2, test="Chisq"))

Data: data

Models:

res.null: winner_analysis ~ 1 + (1 | dyad)

res_ori_m2: winner_analysis ~ rel_nummales + rel_swfempermale + rel_UD190 +

res_ori_m2: (1 | dyad)

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
res.null	2	120.76	125.71	-58.378	116.76				
res_ori_m2	5	114.23	126.62	-52.116	104.23	12.524		3	0.005787 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>

>

> #AIC values to the list

> models[[5]]<-res_ori_m1

> Modnames <- rbind(Modnames, "Model with original male-based variables (no no.males)")

> models[[6]]<-res_ori_m2

> Modnames <- rbind(Modnames, "Model with original male-based variables (no inf. per male)")

>

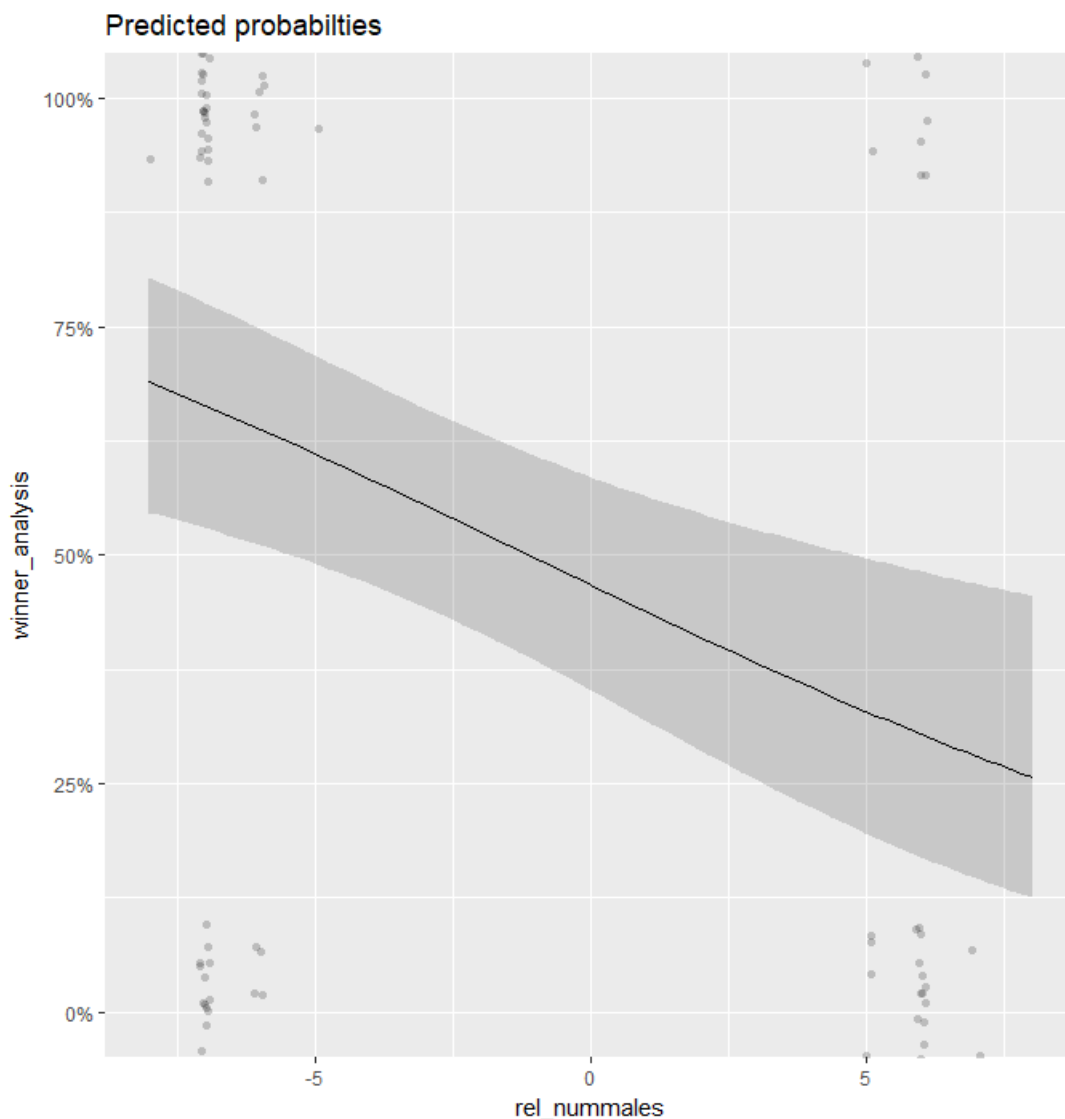
>

> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)

```

> r2_original_m1<-r.squaredGLMM(res_ori_m1)
The result is correct only if all data used by the model has not changed s
ince model was fitted.
> R2<-rbind(R2,r2_original_m1)
>
> r2_original_m2<-r.squaredGLMM(res_ori_m2)
The result is correct only if all data used by the model has not changed s
ince model was fitted.
> R2<-rbind(R2,r2_original_m2)
> #Graphs
> sjp.glmer(res_ori_m2, type="pred", facet.grid=FALSE, vars="rel_nummales"
,geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite

```

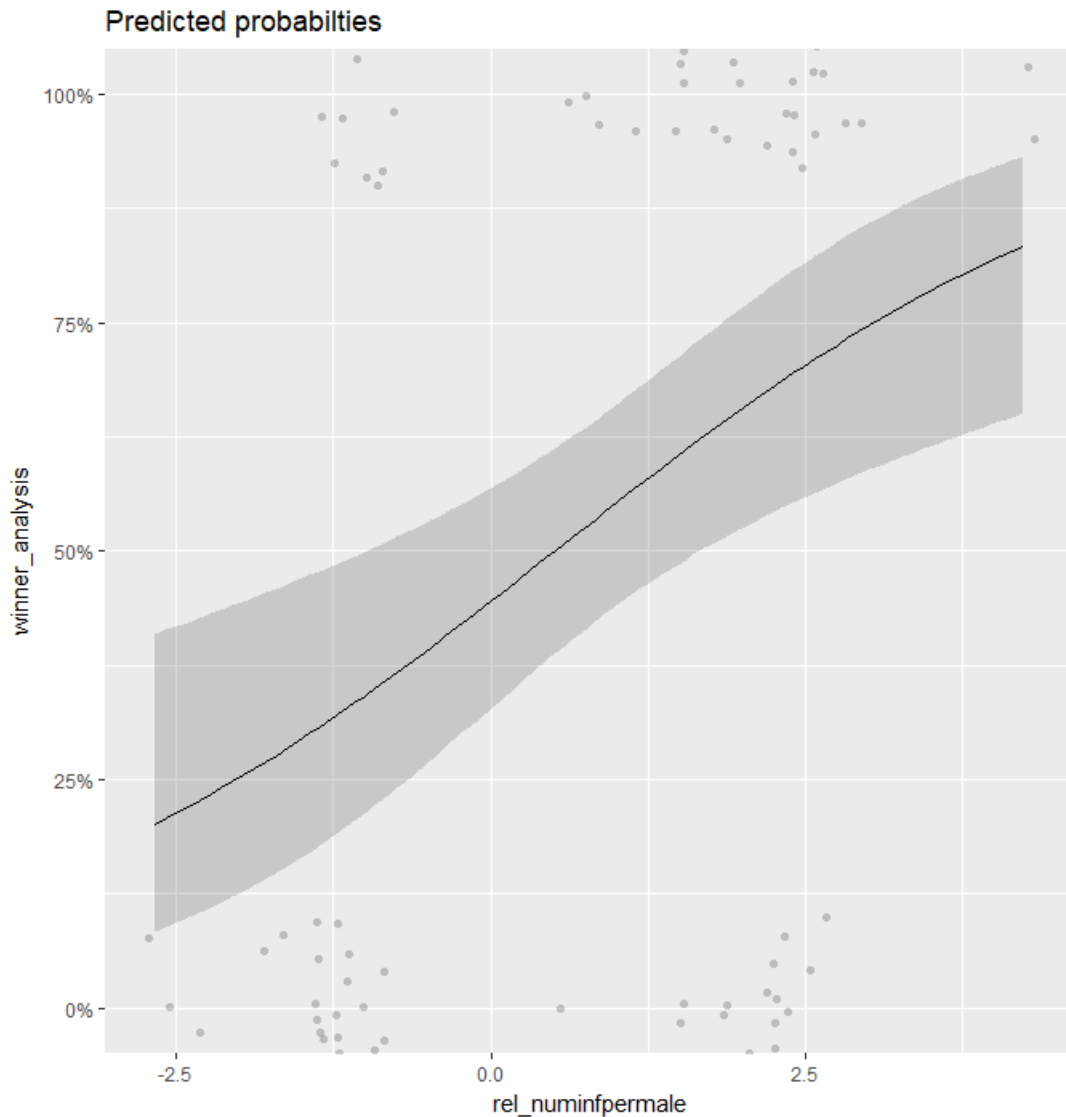


```

> sjp.glmer(res_ori_m1, type="pred", facet.grid=FALSE, vars="rel_numinfper
male",geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite

```

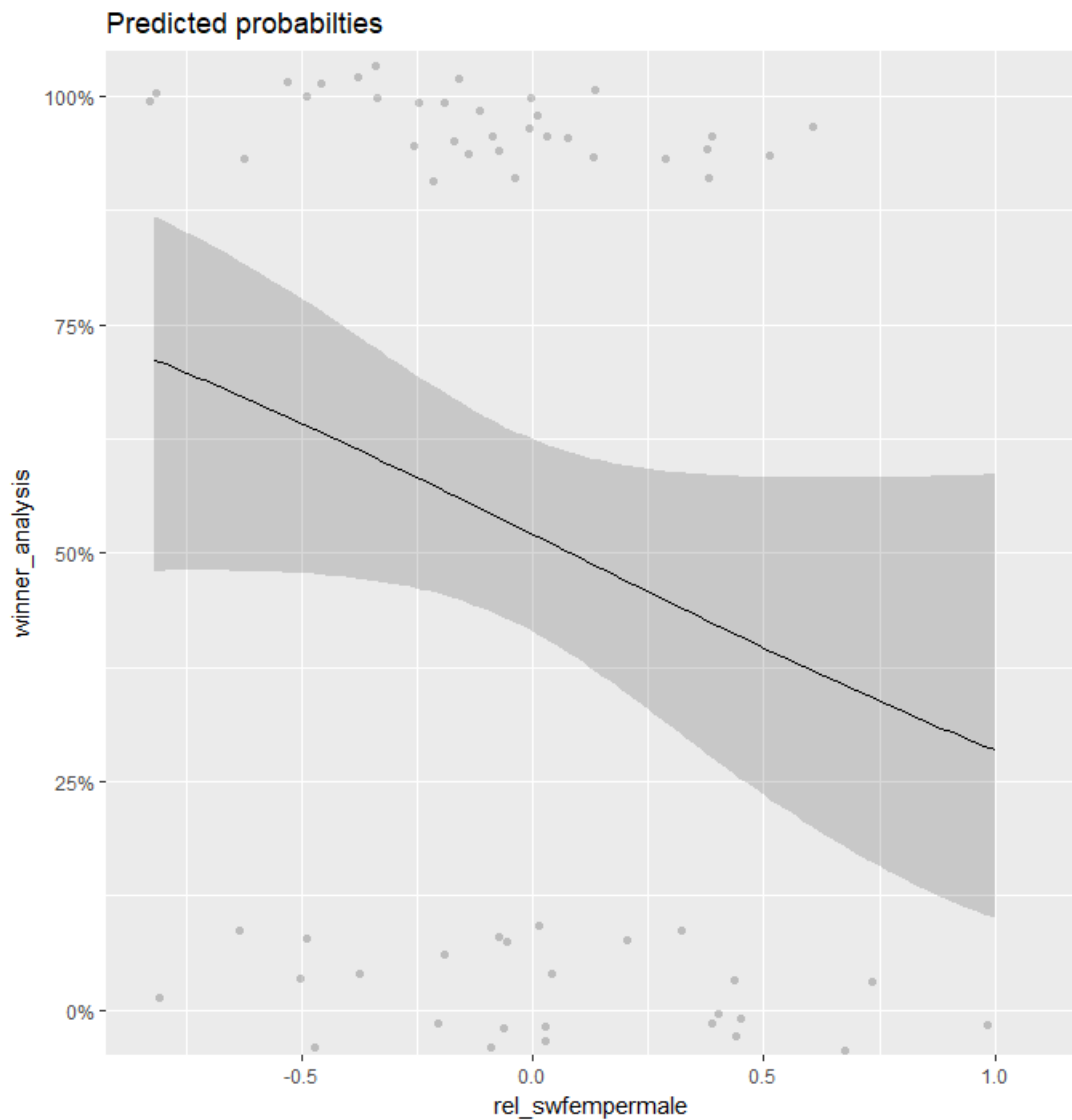
the matrix is either rank-deficient or indefinite



```
> sjp.glmer(res_ori_m2, type="pred", facet.grid=FALSE, vars="rel_swfempermale", geom.colors = "bw", show.ci=TRUE)
```

warning messages:

```
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
```



```
> cat("\n\n\n Male-based model with integer variables as proposed in the
viva n\n\n\n")
```

Male-based model with integer variables as proposed in the viva n

```
>
> #Checking co-linearity (values close to 1 are good, over 4 can be proble
matic)
> vif(glm(winner_analysis ~ rel_nummales+rel_infants+rel_numswfem+rel_UD19
0, family="binomial", data=data))
rel_nummales rel_infants rel_numswfem rel_UD190
1.181199 1.093212 1.134220 1.169259
>
> #Run the model
> res_new_m=glmer(winner_analysis ~
+ rel_nummales+rel_infants+rel_numswfem+rel_UD190+
```

```

+           (1|dyad), family="binomial", data=data)
>
> print(summary(res_new_m))
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_nummales + rel_infants + rel_numswfem +
  rel_UD190 + (1 | dyad)
Data: data

      AIC      BIC   logLik deviance df.resid
    113.7    128.5   -50.8   101.7      82

Scaled residuals:
    Min       1Q   Median       3Q      Max
-1.7797 -0.8017  0.3228  0.6951  2.1860

Random effects:
Groups Name      Variance Std.Dev.
dyad    (Intercept) 0        0
Number of obs: 88, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.493481   0.479890   1.028 0.303798
rel_nummales -0.147532   0.043278  -3.409 0.000652 ***
rel_infants  -0.018452   0.082953  -0.222 0.823973
rel_numswfem -0.158832   0.101708  -1.562 0.118371
rel_UD190     0.018247   0.007228   2.525 0.011584 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

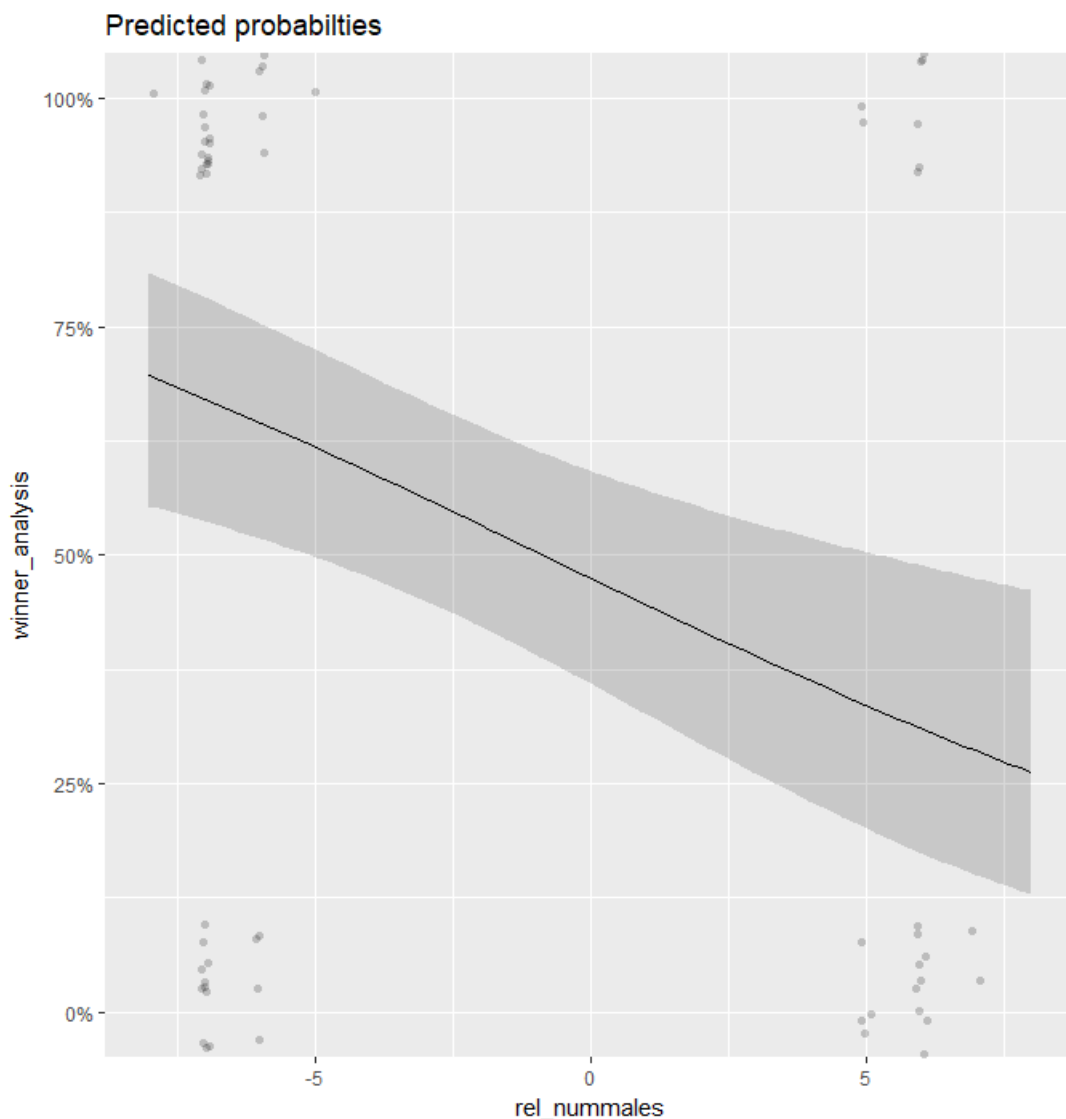
Correlation of Fixed Effects:
              (Intr) r1_nmm r1_nfn r1_nms
rel_nummales  0.015
rel_infants  -0.226 -0.086
rel_numswfem -0.842  0.215  0.222
rel_UD190     0.097 -0.347  0.132 -0.161
>
> cat("\n\n Comparison of male-based model to null model\n\n")

Comparison of male-based model to null model

>
> print(anova(res.null, res_new_m, test="Chisq"))
Data: data
Models:
res.null: winner_analysis ~ 1 + (1 | dyad)
res_new_m: winner_analysis ~ rel_nummales + rel_infants + rel_numswfem +
res_new_m: rel_UD190 + (1 | dyad)
      Df    AIC    BIC   logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 120.76 125.71 -58.378   116.76
res_new_m  6 113.67 128.53 -50.834   101.67 15.088     4   0.004522 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> #AIC values to the list
> models[[7]]<-res_new_m

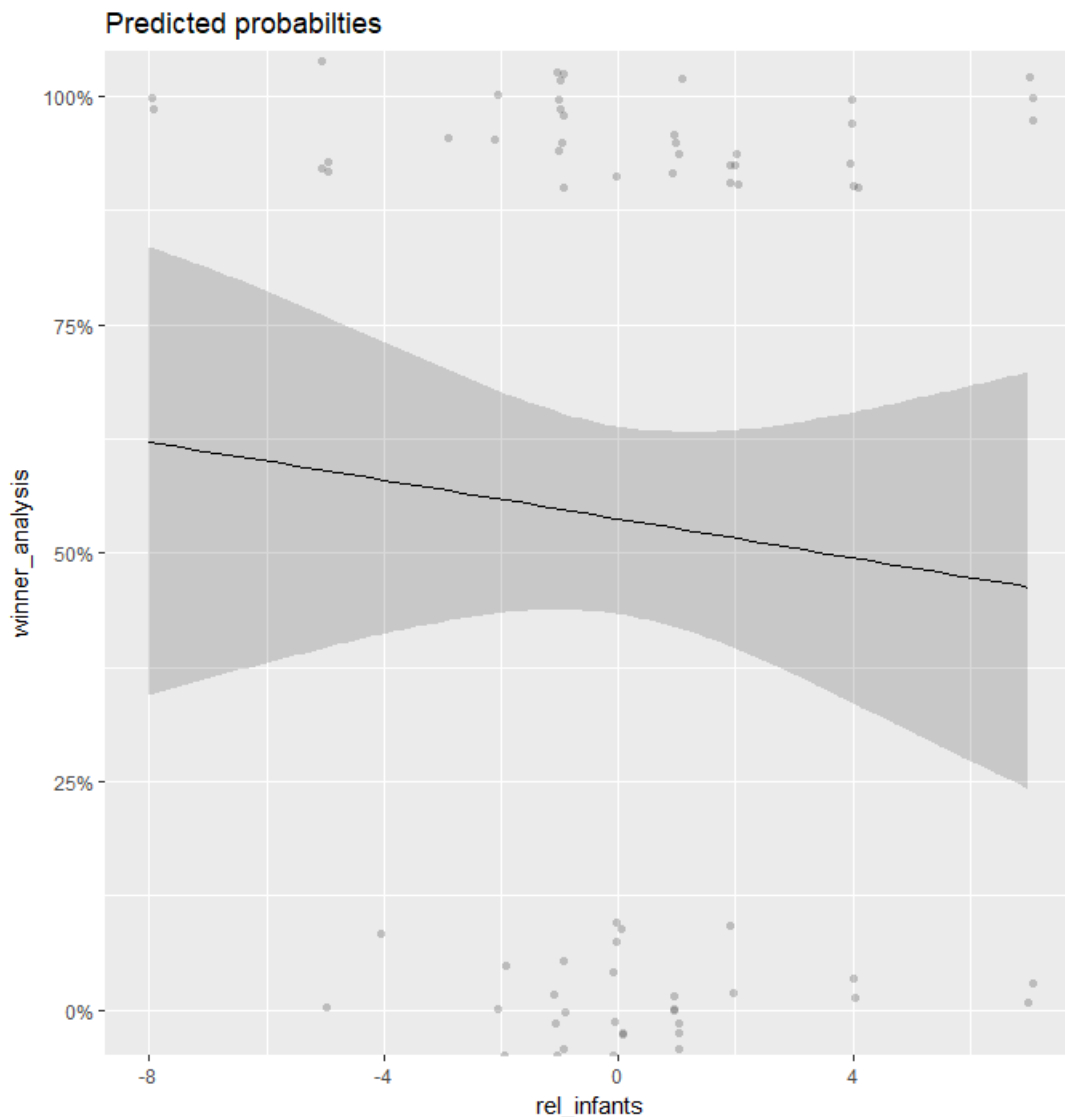
```

```
> Modnames <- rbind(Modnames, "Model with new variables (males)")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_new_m<-r.squaredGLMM(res_new_m)
The result is correct only if all data used by the model has not changed since model was fitted.
> R2<-rbind(R2,r2_new_m)
>
>
> sjp.glmer(res_new_m, type="pred", facet.grid=FALSE, vars="rel_nummales", geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
```



```
> sjp.glmer(res_new_m, type="pred", facet.grid=FALSE, vars="rel_infants", geom.colors = "bw",show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model()` instead.
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
```

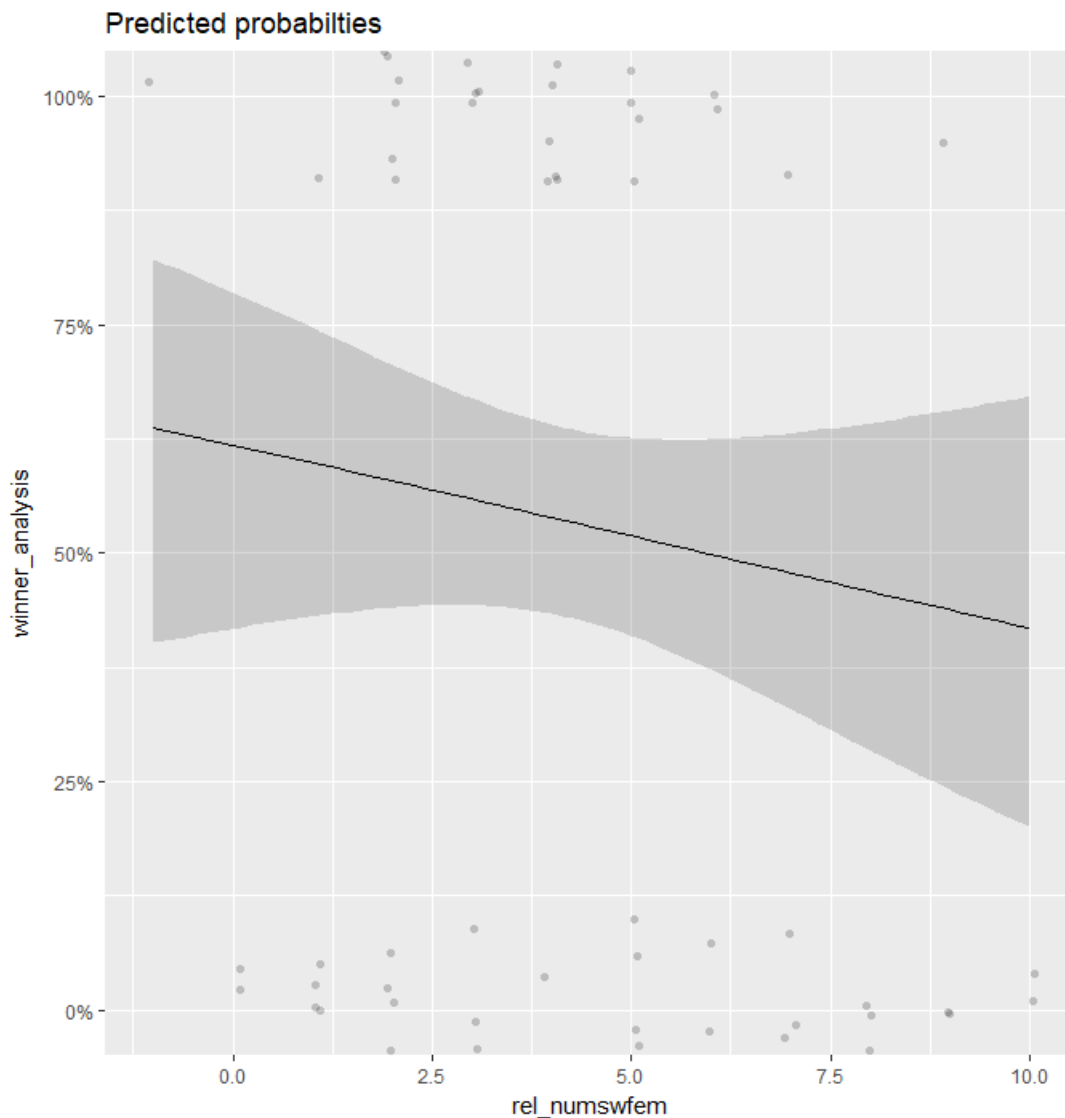
the matrix is either rank-deficient or indefinite
 2: In chol.default(sigma, pivot = TRUE) :
 the matrix is either rank-deficient or indefinite



```
> sjp.glmer(res_new_m, type="pred", facet.grid=FALSE, vars="rel_numswfem",
  geom.colors = "bw", show.ci=TRUE)
```

warning messages:

```
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
```



```
> #####
#####
> #####
#####
> #####
#####
> cat("\n\n RESULTS \n\n")
```

RESULTS

```
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = N
ULL, sort = TRUE)
```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcwt	Cum.Wt
LL					
Model with original male-based variables (no no.males)	5	113.66	0.00	0.45	0.45
-51.47					

Model with new variables (males)	6	114.71	1.04	0.27	0.72
-50.83					
Model with original male-based variables (no inf. per male)	5	114.96	1.30	0.24	0.96
-52.12					
Model with new variables	6	120.20	6.53	0.02	0.97
-53.58					
Model with original variables	6	120.63	6.97	0.01	0.99
-53.80					
null model	2	120.90	7.23	0.01	1.00
-58.38					

Warning message:

```
In data.row.names(row.names, rowsi, i) :
  some row.names duplicated: 3,4,5,6 --> row.names NOT used
> R2
```

	R2m	R2c
R2	0.0000000	0.1162905
r2_original	0.1393451	0.2333535
r2_new	0.1460438	0.2372488
r2_original_m1	0.2739379	0.2739379
r2_original_m2	0.2444607	0.2444607
r2_new_m	0.2878664	0.2878664

#Male-based original variables 1
#Male-based original variables 2
#Male-based new variables 1

Male-based models using relative values of integer and ratio variables are equivalent in trends shown, AICc and R^2 despite the fact that with original variables there is high co-linearity between 2 fixed effects and 2 models are needed

```
> #####
#####
> #####
#####
> #####
#####
> cat("\n\n\n Original ratio variables & new integer variables when using
absolute values \n\n\n")
```

Original ratio variables & new integer variables when using absolute values

```

>
> ## Upload data
> data<-read.csv("Data_for_revision_subsample.csv")
>
>
>
>
>
> ###Convert variables to the appropriate format
> data$num_obs<- as.numeric(data$num_obs)
> data$dyad<- factor(data$dyad)
> data$durationIGE<- as.numeric(data$durationIGE)
> data$abs_numfemales<- as.numeric(data$abs_numfemales)
> data$abs_infants<- as.numeric(data$abs_infants)
> data$abs_numinfperfem<- as.numeric(data$abs_numinfperfem)
> data$abs_numswfem<- as.numeric(data$abs_numswfem)
> data$abs_swfemperfem<- as.numeric(data$abs_swfemperfem)
> data$abs_UD190<- as.numeric(data$abs_UD190)
> data$decided_undecided<- as.factor(data$decided_undecided)
> data$aggression_yn<- as.factor(data$aggression_yn)
> data$aggression_level<- as.factor(data$aggression_level)
>
> #Eliminating NAs (otherwise when calculating the null models the sample
size is different and the comparison cannot be made)
> missingrows = is.na(data$abs_numfemales)
> data= data[!missingrows,]
> missingrows = is.na(data$abs_numinfperfem)
> data= data[!missingrows,]
> missingrows = is.na(data$abs_swfemperfem)
> data= data[!missingrows,]
>
>
>
> cat("\n\n\n\n\n\n\n  Decided IGE VS Draws \n\n\n\n\n\n\n")

```

Decided IGE VS Draws

```

>
> cat("\n\n\n\n\n\n\n Checking correlations between fixed effects \n\n\n\n\n\n\n")

```

Checking correlations between fixed effects

```

>
> #Correlations between variables used in the original models (abs_numfemales,
abs_numinfperfem and abs_swfemperfem and abs_UD190)
> dataf_original<-data.frame(data$abs_numfemales,data$abs_numinfperfem,data$abs_swfemperfem,data$abs_UD190)
> pcor(dataf_original)

```

```

$estimate
      data.abs_numfemales data.abs_numinfperfem data.abs_swfemperfem data.abs
_UD190
data.abs_numfemales      1.00000000      -0.09918152      0.04374948     -0.03
976766
data.abs_numinfperfem    -0.09918152      1.00000000      0.31372942      0.02
438933
data.abs_swfemperfem      0.04374948      0.31372942      1.00000000      0.07
994083
data.abs_UD190           -0.03976766      0.02438933      0.07994083      1.00
000000

$p.value
      data.abs_numfemales data.abs_numinfperfem data.abs_swfemperfem data.abs
_UD190
data.abs_numfemales      0.00000000      0.3094389233      0.6545522955      0.6
842363
data.abs_numinfperfem      0.3094389      0.0000000000      0.0009996775      0.8
030830
data.abs_swfemperfem      0.6545523      0.0009996775      0.0000000000      0.4
130644
data.abs_UD190           0.6842363      0.8030830251      0.4130643511      0.0
000000

$statistic
      data.abs_numfemales data.abs_numinfperfem data.abs_swfemperfem data.abs
_UD190
data.abs_numfemales      0.00000000      -1.0213440      0.4487284      -0.4
078198
data.abs_numinfperfem     -1.0213440      0.00000000      3.3857060      0.2
499907
data.abs_swfemperfem      0.4487284      3.3857060      0.00000000      0.8
217798
data.abs_UD190           -0.4078198      0.2499907      0.8217798      0.0
000000

$n
[1] 109

$gp
[1] 2

$method
[1] "pearson"

>
>
> #Correlations between the new variables (abs_infants, abs_numswfem) and
those which don't change (abs_numfemales and abs_UD190)
> dataf_new<-data.frame(data$abs_numfemales,data$abs_infants, data$abs_num
swfem,data$abs_UD190)
> pcor(dataf_new)
$estimate
      data.abs_numfemales data.abs_infants data.abs_numswfem data.abs_UD190
data.abs_numfemales      1.00000000      0.09093854      0.09559512     -0.05249961
data.abs_infants        0.09093854      1.00000000     -0.23098683      0.05515327
data.abs_numswfem       0.09559512     -0.23098683      1.00000000      0.09701175
data.abs_UD190         -0.05249961      0.05515327      0.09701175      1.00000000

$p.value

```

	data.abs_numfemales	data.abs_infants	data.abs_numswfem	data.abs_UD190
data.abs_numfemales	0.0000000	0.35156454	0.32734558	0.5912315
data.abs_infants	0.3515645	0.00000000	0.01667716	0.5725917
data.abs_numswfem	0.3273456	0.01667716	0.00000000	0.3201947
data.abs_UD190	0.5912315	0.57259173	0.32019473	0.0000000

\$statistic

	data.abs_numfemales	data.abs_infants	data.abs_numswfem	data.abs_UD190
data.abs_numfemales	0.0000000	0.9357199	0.9840652	-0.5387038
data.abs_infants	0.9357199	0.0000000	-2.4326984	0.5660143
data.abs_numswfem	0.9840652	-2.4326984	0.0000000	0.9987857
data.abs_UD190	-0.5387038	0.5660143	0.9987857	0.0000000

\$n

[1] 109

\$gp

[1] 2

\$method

[1] "pearson"

```
>
>
>
>
> cat("\n\n Null model \n\n")
```

Null model

```
>
> res.null=glmer(decided_undecided ~ 1+ (1|dyad), family="binomial", data
=data)
>
> #AIC values to the list
> models<-list()
> models[[1]]<-res.null
> Modnames <- "null model"
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Sch
ielzeth, 2013)
> r2_null<-r.squaredGLMM(res.null)
The result is correct only if all data used by the model has not changed s
ince model was fitted.
> R2<-r2_null
>
>
> cat("\n\n\n\n\n\n\n\n Using original variables (Proportions of tumescent
females and infants per female) \n\n\n\n\n\n\n\n\n")
```

Using original variables (Proportions of tumescent females and infants pe
r female)

```

>
>
> #Checking co-linearity (values close to 1 are good, over 4 can be problematic)
> vif(glm(decided_undecided ~ abs_numfemales+abs_numinfperfem+abs_swfemper
fem+abs_UD190, family="binomial", data=data))
      abs_numfemales abs_numinfperfem abs_swfemperfem      abs_UD190
      1.024462      1.054136      1.079804      1.027092
>
> #Run the model
> res_original=glmer(decided_undecided ~ abs_numfemales+abs_numinfperfem+a
bs_swfemperfem+abs_UD190+(1|dyad), family="binomial", data=data)
>
> print(summary(res_original))
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: binomial ( logit )
Formula: decided_undecided ~ abs_numfemales + abs_numinfperfem + abs_swfem
perfem +      abs_UD190 + (1 | dyad)
Data: data

      AIC      BIC    logLik deviance df.resid
    110.0    126.1    -49.0     98.0     103

Scaled residuals:
      Min       1Q   Median       3Q      Max
-3.1203  0.2769  0.3639  0.5042  1.2833

Random effects:
Groups Name      Variance Std.Dev.
dyad   (Intercept) 2.778e-16 1.667e-08
Number of obs: 109, groups: dyad, 3

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -0.96176    1.14738  -0.838  0.40191
abs_numfemales  0.35876    0.13880   2.585  0.00975 **
abs_numinfperfem -1.90907    2.58206  -0.739  0.45969
abs_swfemperfem -1.36482    2.81729  -0.484  0.62807
abs_UD190       0.01315    0.01072   1.227  0.21998
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

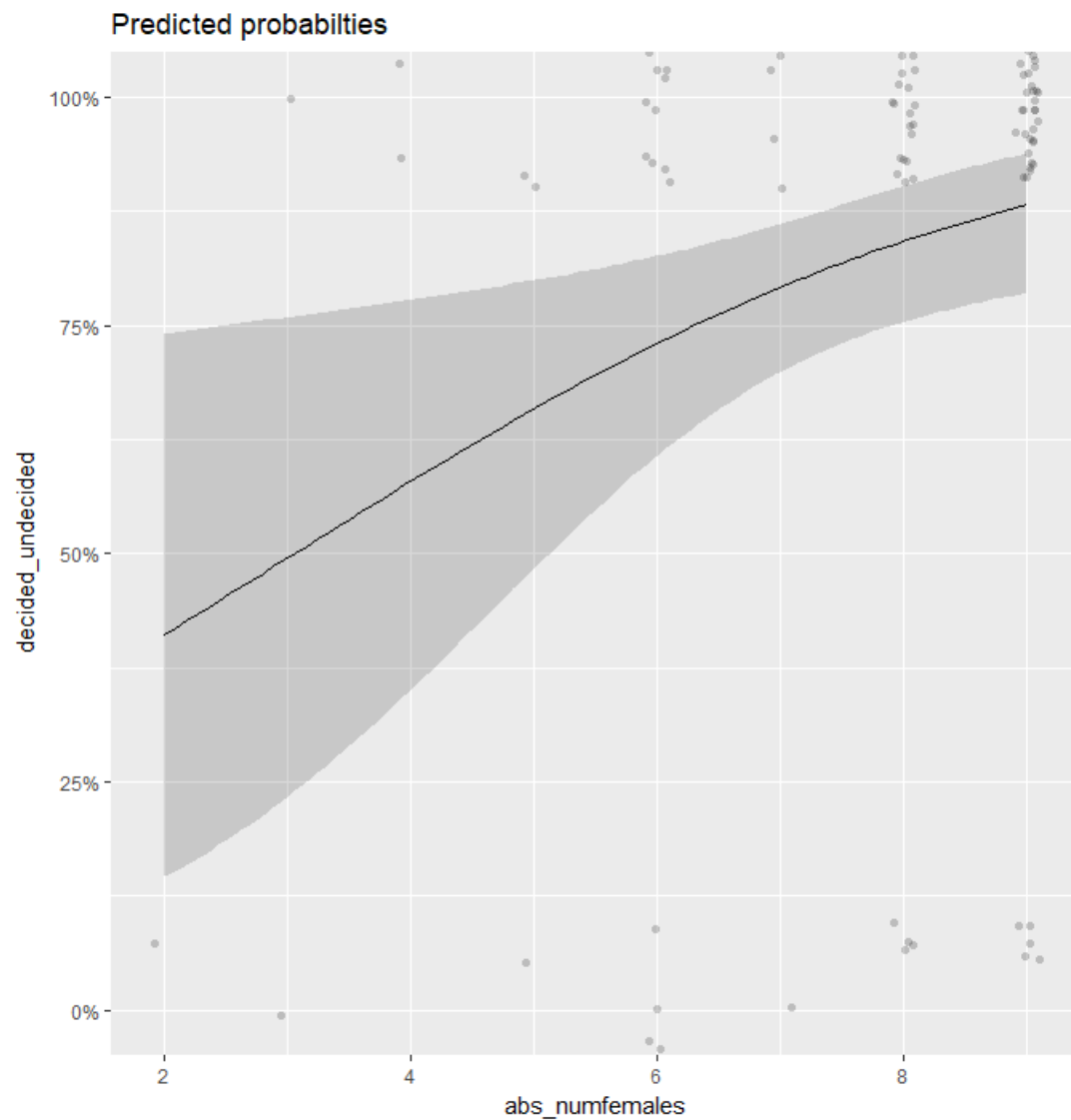
Correlation of Fixed Effects:
              (Intr) abs_nmf abs_nmn abs_sw
abs_numfmls  -0.822
abs_nmnfprf  -0.344 -0.013
abs_swfmpfrf -0.128 -0.124 -0.211
abs_UD190    -0.246  0.100 -0.051 -0.116
>
> cat("\n\n Comparison of model with original variables and model to nul
l model\n\n")

```

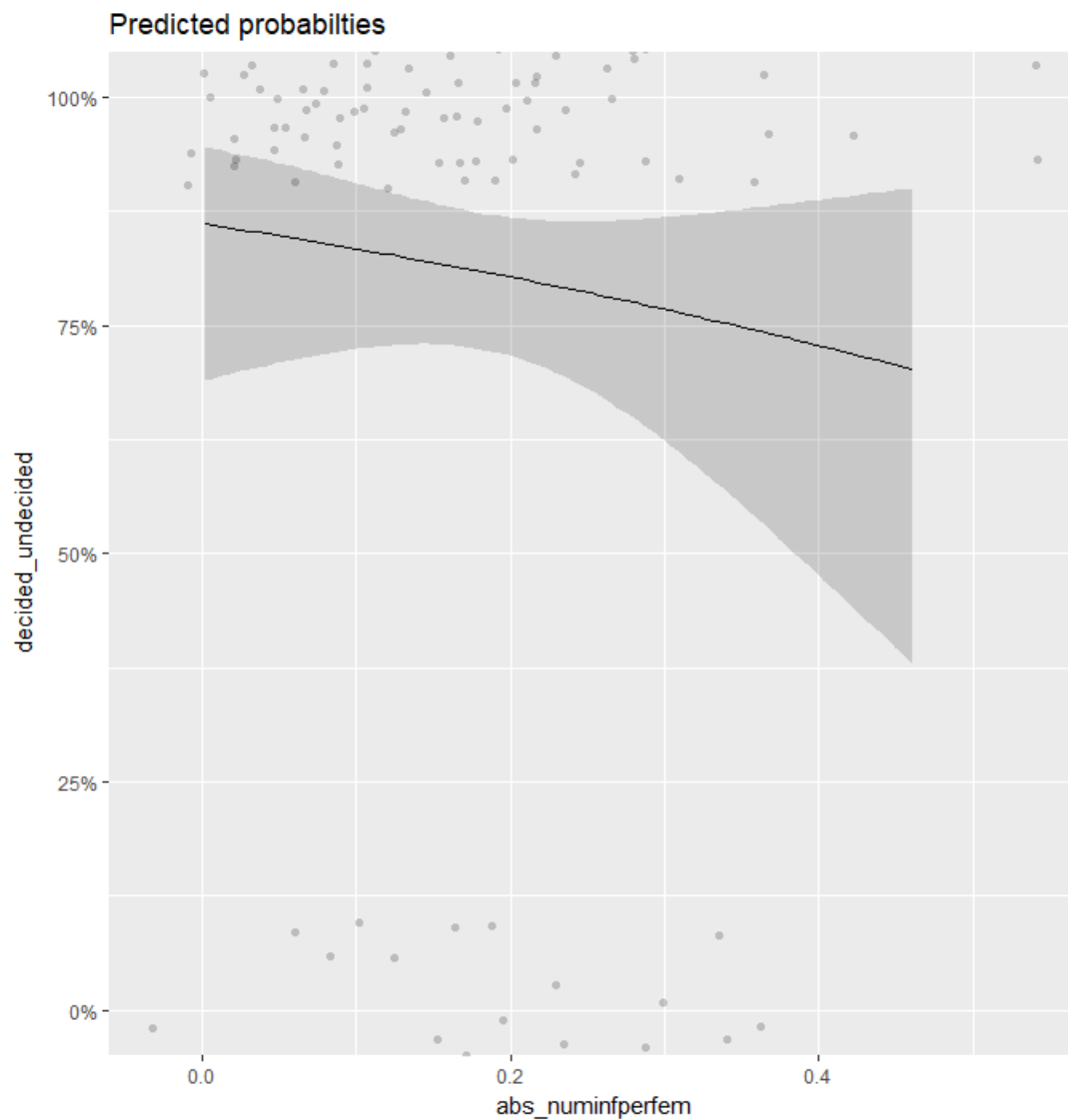
comparison of model with original variables and model to null model

```
>
> print(anova(res.null,res_original, test="Chisq"))
Data: data
Models:
res.null: decided_undecided ~ 1 + (1 | dyad)
res_original: decided_undecided ~ abs_numfemales + abs_numinfperfem + abs_
swfemperfem +
res_original:      abs_UD190 + (1 | dyad)
      Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null      2 110.83 116.22 -53.416  106.833
res_original  6 109.95 126.10 -48.976   97.951 8.8814      4    0.06413 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> #AIC values to the list
> models[[2]]<-res_original
> Modnames <- rbind(Modnames, "Model with original variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Sch
ielzeth, 2013)
> r2_original<-r.squaredGLMM(res_original)
The result is correct only if all data used by the model has not changed s
ince model was fitted.
> R2<-rbind(R2,r2_original)
>
>
>
>
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_numfema
les",geom.colors = "bw",show.ci=TRUE)
```

``sjp.glmer()`` will become deprecated in the future. Please use ``plot_model()`` instead.

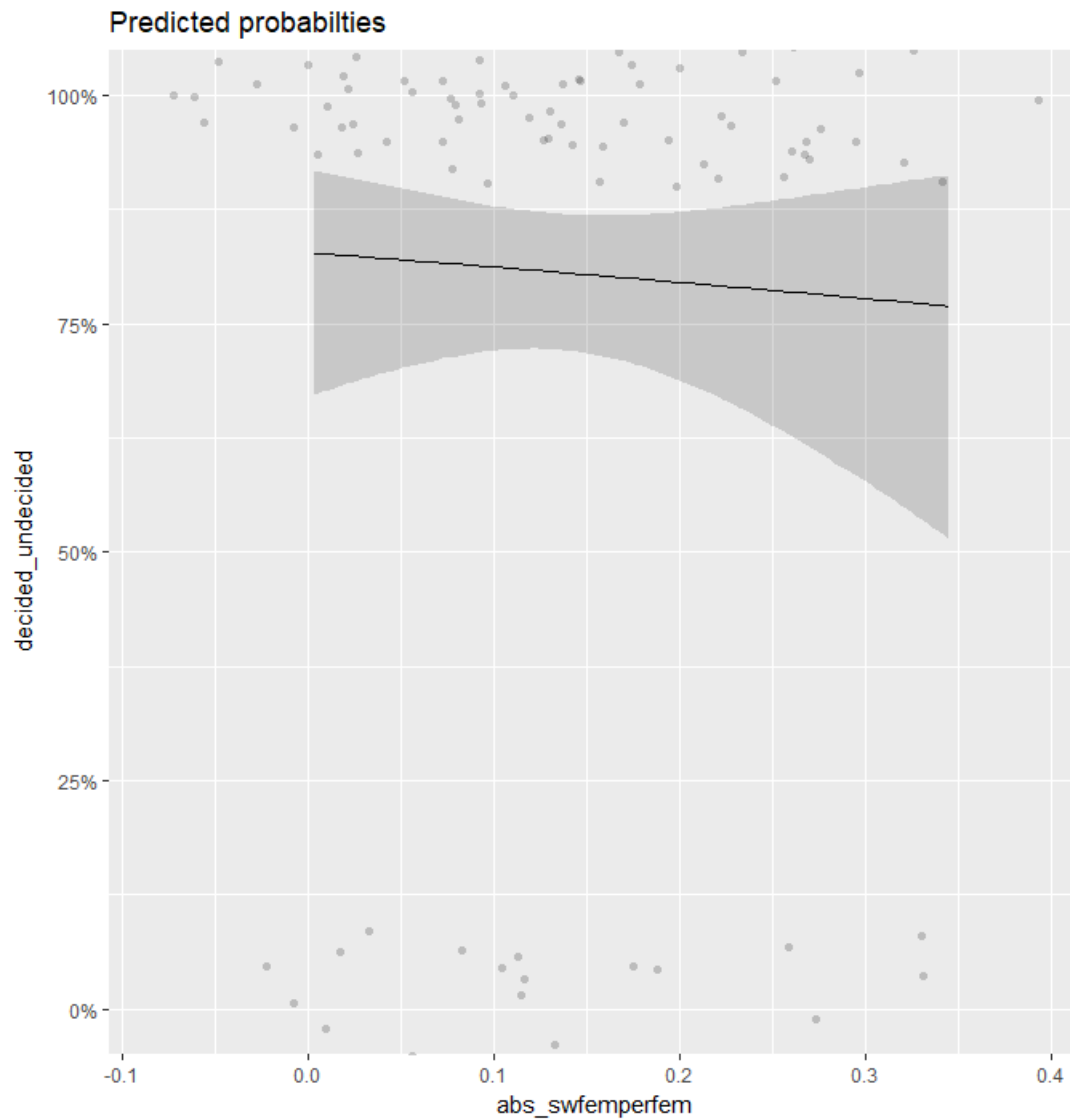


```
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_numinfperferfem",geom.colors = "bw",show.ci=TRUE)
```



```
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_swfempe  
rfem",geom.colors = "bw",show.ci=TRUE)
```


``sjp.glmer()`` will become deprecated in the future. Please use ``plot_model()`` instead.



```
>
>
>
> cat("\n\n\n\n\n\n\n\n Variables proposed in viva (No.infants/Females with infants and No. tumescent females) \n\n\n\n\n\n\n\n\n")
```

Variables proposed in viva (No.infants/Females with infants and No. tumescent females)

```

>
> #Checking co-linearity (values close to 1 are good, over 4 can be problematic)
> vif(glm(decided_undecided ~ abs_numfemales+abs_infants+abs_numswfem+abs_UD190, family="binomial", data=data))
abs_numfemales    abs_infants    abs_numswfem    abs_UD190
      1.045287      1.055123      1.098188      1.023908
>
> #Run the model
> res_new=glmer(decided_undecided ~
+             abs_numfemales+abs_infants+abs_numswfem+abs_UD190+
+             (1|dyad), family="binomial", data=data)
>
> print(summary(res_new))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial (logit)
Formula: decided_undecided ~ abs_numfemales + abs_infants + abs_numswfem + abs_UD190 + (1 | dyad)
Data: data

      AIC      BIC    logLik deviance df.resid
  110.7   126.9   -49.4    98.7     103

Scaled residuals:
    Min       1Q   Median       3Q      Max
-3.0657  0.3036  0.3794  0.4958  1.1661

Random effects:
Groups Name      Variance Std.Dev.
dyad  (Intercept) 0        0
Number of obs: 109, groups: dyad, 3

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)  -1.30286    1.09222  -1.193  0.23292
abs_numfemales  0.36162    0.13829   2.615  0.00893 **
abs_infants   -0.01025    0.12358  -0.083  0.93387
abs_numswfem  -0.04642    0.09811  -0.473  0.63610
abs_UD190      0.01267    0.01090   1.162  0.24522
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) abs_nmf abs_nf abs_nms
abs_numfmls  -0.816
abs_infants  -0.249 -0.090
abs_numswfm  -0.243 -0.190  0.222
abs_UD190    -0.259  0.096 -0.057 -0.133
>
> cat("\n\n Comparison of female-based (new) model to null model\n\n")

Comparison of female-based (new) model to null model

>
> print(anova(res.null,res_new, test="Chisq"))

```

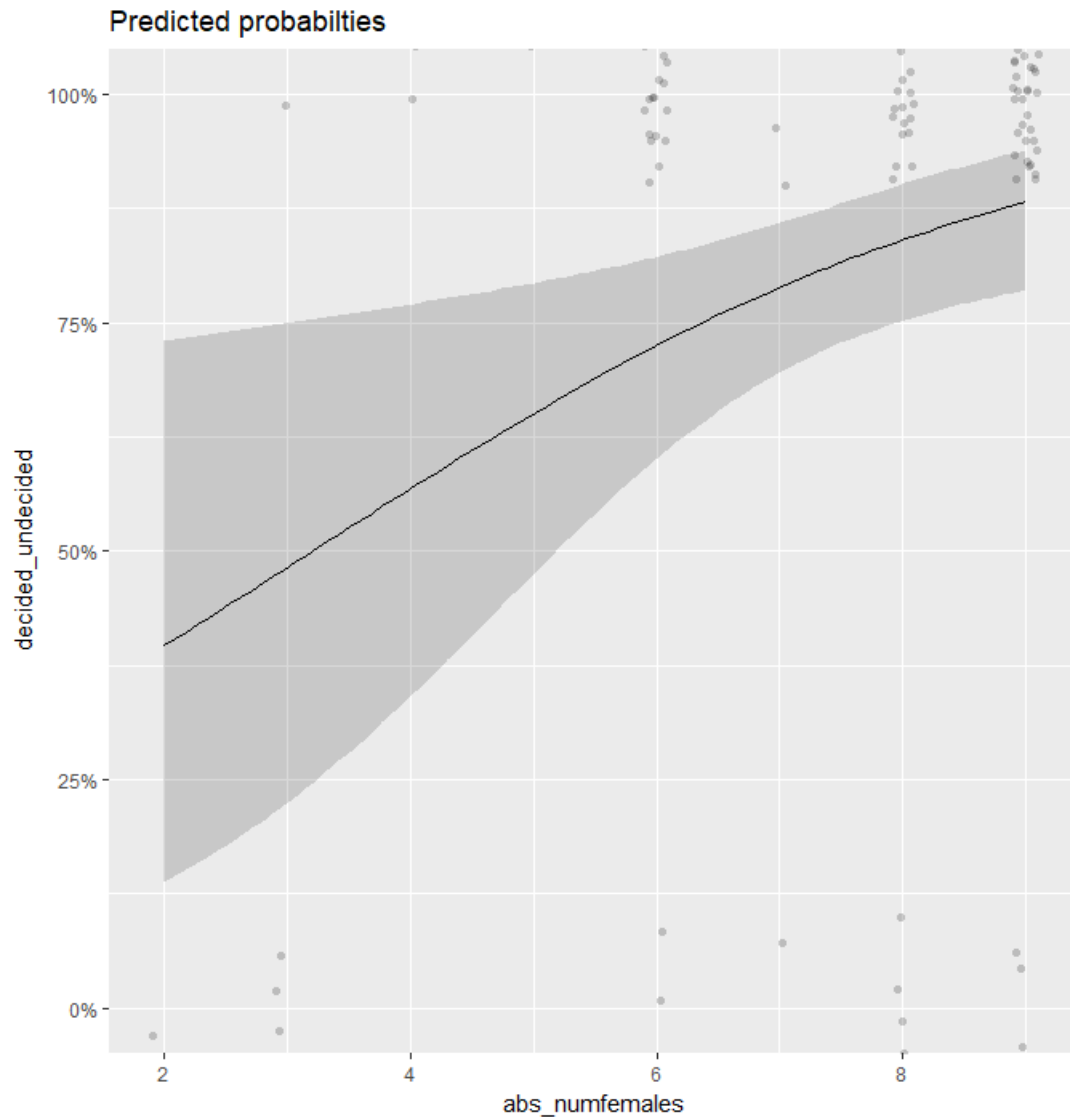
```

Data: data
Models:
res.null: decided_undecided ~ 1 + (1 | dyad)
res_new: decided_undecided ~ abs_numfemales + abs_infants + abs_numswfem +

res_new:      abs_UD190 + (1 | dyad)
      Df      AIC      BIC  logLik deviance  Chisq Chi Df Pr(>Chisq)
res.null  2 110.83 116.22 -53.416 106.833
res_new   6 110.71 126.86 -49.357  98.713 8.1193      4    0.0873 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
> #AIC values to the list
> models[[3]]<-res_new
> Modnames <- rbind(Modnames, "Model with new variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_new<-r.squaredGLMM(res_new)
The result is correct only if all data used by the model has not changed since model was fitted.
> R2<-rbind(R2,r2_new)
>
>
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_numfemales",
geom.colors = "bw",show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model()` instead.
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :

```

the matrix is either rank-deficient or indefinite

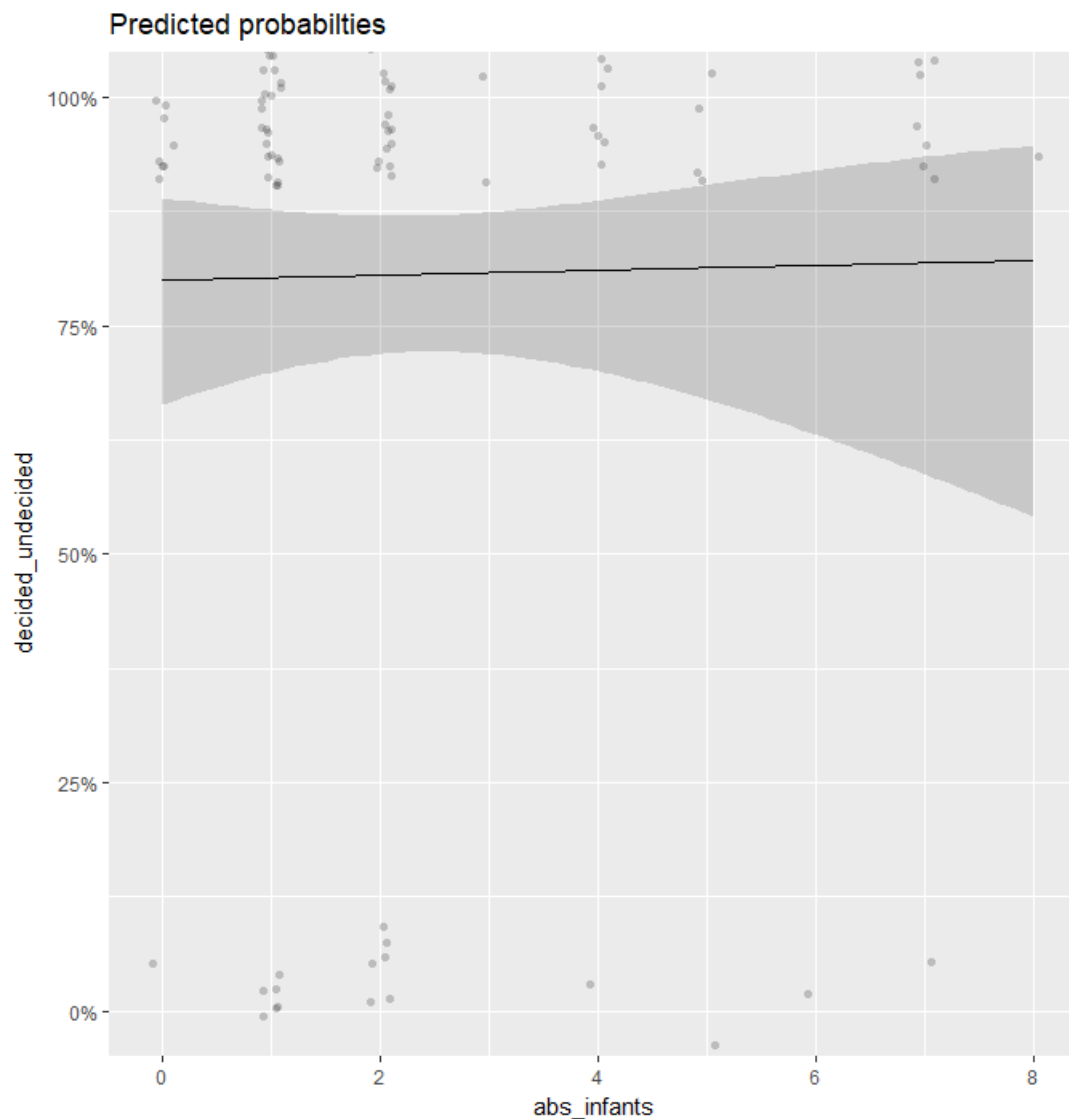


```
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_infants", geo
m.colors = "bw", show.ci=TRUE)
```

Warning messages:

- 1: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 2: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 3: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite

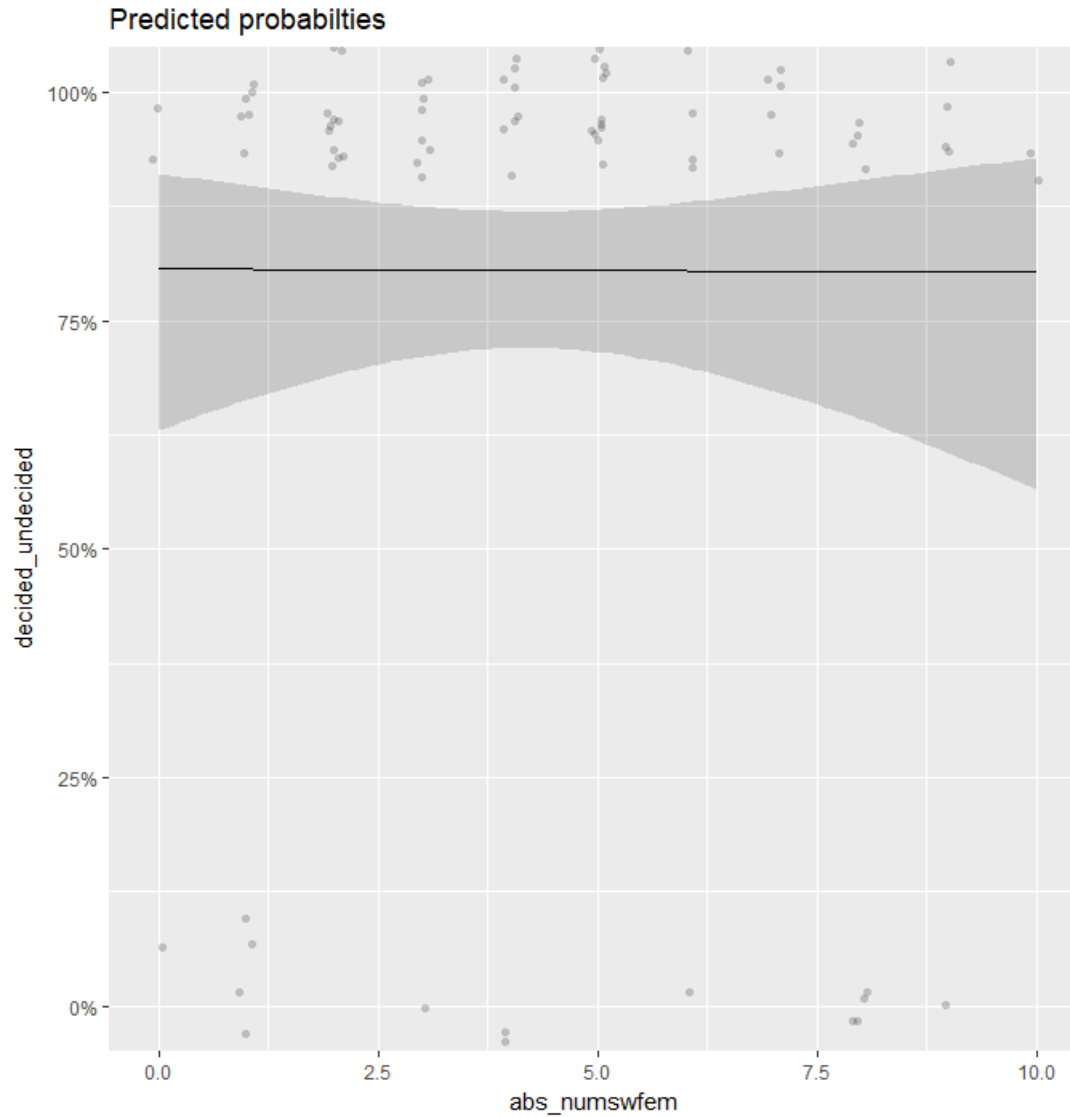
```
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_numswfem", geom.colors = "bw", show.ci=TRUE)
```



Warning messages:

- 1: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 2: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 3: In chol.default(sigma, pivot = TRUE) :

the matrix is either rank-deficient or indefinite



```
>
>
>
> #####
> #####
> #####
> #####
> cat("\n\n RESULTS \n\n")
```

RESULTS

```
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = N
ULL, sort = TRUE)
```

Model selection based on AICc:

K	AICc	Delta_AICc	AICcwt	Cum.Wt	LL
---	------	------------	--------	--------	----

Model with original variables	6	110.77	0.00	0.38	0.38	-48.98
null model	2	110.95	0.17	0.35	0.74	-53.42
Model with new variables	6	111.54	0.76	0.26	1.00	-49.36

Warning message:

```
In data.row.names(row.names, rowsi, i) :
  some row.names duplicated: 3 --> row.names NOT used
> R2
```

	R2m	R2c
R2	0.0000000	0.0000000
r2_original	0.1404039	0.1404039
r2_new	0.1223804	0.1223804

```
> cat("\n\n\n\n\n\n\n  AGGRESSION YES/NO \n\n\n\n\n\n\n")
```

AGGRESSION YES/NO

```
>
> ## Upload data
> data<-read.csv("Data_for_revision_subsample.csv")
>
>
>
>
>
>
> ###Convert variables to the appropriate format
> data$num_obs<- as.numeric(data$num_obs)
> data$dyad<- factor(data$dyad)
> data$durationIGE<- as.numeric(data$durationIGE)
> data$abs_numfemales<- as.numeric(data$abs_numfemales)
> data$abs_infants<- as.numeric(data$abs_infants)
> data$abs_numinfperfem<- as.numeric(data$abs_numinfperfem)
> data$abs_numswfem<- as.numeric(data$abs_numswfem)
> data$abs_swfemperfem<- as.numeric(data$abs_swfemperfem)
> data$abs_UD190<- as.numeric(data$abs_UD190)
> data$decided_undecided<- as.factor(data$decided_undecided)
> data$aggression_yn<- as.factor(data$aggression_yn)
> data$aggression_level<- as.factor(data$aggression_level)
>
> #Eliminating NAs (otherwise when calculating the null models the sample
size is different and the comparison cannot be made)
> missingrows = is.na(data$abs_numfemales)
> data= data[!missingrows,]
> missingrows = is.na(data$abs_numinfperfem)
> data= data[!missingrows,]
> missingrows = is.na(data$abs_swfemperfem)
> data= data[!missingrows,]
> missingrows = is.na(data$aggression_yn)
> data= data[!missingrows,]
>
```

```

>
> cat("\n\n Null model \n\n")

Null model

>
> res.null=glmer(aggression_yn ~ durationIGE+ (1|dyad), family="binomial"
, data=data)
>
> #AIC values to the list
> models<-list()
> models[[1]]<-res.null
> Modnames <- "null model"
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Sch
ielzeth, 2013)
> r2_null<-r.squaredGLMM(res.null)
The result is correct only if all data used by the model has not changed s
ince model was fitted.
> R2<-r2_null
>
>
> cat("\n\n\n\n\n\n\n\n Using original variables (Proportions of tumescent
females and infants per female) \n\n\n\n\n\n\n\n\n")

```

Using original variables (Proportions of tumescent females and infants pe
r female)

```

>
>
> #Checking co-linearity (Values close to 1 are good, over 4 can be proble
matic)
> vif(glm(aggression_yn ~ abs_numfemales+abs_numinfperfem+abs_swfemperfem+
abs_UD190+durationIGE, family="binomial", data=data))
abs_numfemales abs_numinfperfem abs_swfemperfem abs_UD190 d
urationIGE
1.038749 1.229992 1.213876 1.023329
1.034263
>
> #Run the model
> res_original=glmer(aggression_yn ~ abs_numfemales+abs_numinfperfem+abs_s
wfemperfem+abs_UD190+durationIGE+(1|dyad), family="binomial", data=data)
Warning message:
Some predictor variables are on very different scales: consider rescaling
>

```



```

> print(summary(res_original))
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: binomial ( logit )
Formula: aggression_yn ~ abs_numfemales + abs_numinfperfem + abs_swfemperf
em +      abs_UD190 + durationIGE + (1 | dyad)
Data: data

      AIC      BIC    logLik deviance df.resid
    85.2    104.1    -35.6     71.2     102

Scaled residuals:
    Min       1Q   Median       3Q      Max
-4.0477  0.0160  0.1783  0.4850  1.1283

Random effects:
Groups Name      Variance Std.Dev.
dyad      (Intercept) 0        0
Number of obs: 109, groups: dyad, 3

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.897428   1.965743   0.965  0.33442
abs_numfemales -0.241555   0.206954  -1.167  0.24313
abs_numinfperfem -1.731877   3.272341  -0.529  0.59663
abs_swfemperfem -0.672077   3.495603  -0.192  0.84754
abs_UD190      -0.001646   0.012031  -0.137  0.89121
durationIGE      0.031482   0.010740   2.931  0.00337 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) abs_nmf abs_nmn abs_sw a_UD19
abs_numfmls  -0.905
abs_nmnfprf  -0.282  0.137
abs_swfmpfrf -0.028 -0.096 -0.394
abs_UD190    -0.152  0.036 -0.037 -0.103
durationIGE  -0.326  0.111 -0.093 -0.035 -0.043
fit warnings:
Some predictor variables are on very different scales: consider rescaling
>
> cat("\n\n Comparison of model with original variables and model to nul
l model\n\n")

```

Comparison of model with original variables and model to null model

```

>
> print(anova(res.null,res_original, test="Chisq"))
Data: data
Models:
res.null: aggression_yn ~ durationIGE + (1 | dyad)
res_original: aggression_yn ~ abs_numfemales + abs_numinfperfem + abs_swfe
mperfem +
res_original:      abs_UD190 + durationIGE + (1 | dyad)
      Df      AIC      BIC    logLik deviance Chisq Chi Df Pr(>Chisq)
res.null      3 79.328  87.402  -36.664   73.328
res_original  7 85.211 104.051  -35.606   71.211 2.117      4      0.7143
>

```

```

> #AIC values to the list
> models[[2]]<-res_original
> Modnames <- rbind(Modnames, "Model with original variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_original<-r.squaredGLMM(res_original)
The result is correct only if all data used by the model has not changed since model was fitted.
Warning message:
Some predictor variables are on very different scales: consider rescaling
> R2<-rbind(R2,r2_original)
>
>
>
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_numfemales",geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_numinfperfem",geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_swfemperfem",geom.colors = "bw",show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model()` instead.
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="durationIGE",geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
>
>
>
> cat("\n\n\n\n\n\n\n\n\n variables proposed in viva (No.infants/Females with infants and No. tumescent females) \n\n\n\n\n\n\n\n\n")

```

Variables proposed in viva (No.infants/Females with infants and No. times cent females)

```
>
> #Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
> vif(glm(aggression_yn ~ abs_numfemales+abs_infants+abs_numswfem+abs_UD190+durationIGE, family="binomial", data=data))
```

abs_numfemales	abs_infants	abs_numswfem	abs_UD190	durationIGE
1.068016	1.118682	1.114330	1.013307	1.023539

```
>
> #Run the model
> res_new=glmer(aggression_yn ~
+               abs_numfemales+abs_infants+abs_numswfem+abs_UD190+durationIGE+
+               (1|dyad), family="binomial", data=data)
>
> print(summary(res_new))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: aggression_yn ~ abs_numfemales + abs_infants + abs_numswfem + abs_UD190 + durationIGE + (1 | dyad)
Data: data
```

AIC	BIC	logLik	deviance	df.resid
84.6	103.5	-35.3	70.6	102

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2589	0.0194	0.1910	0.4662	1.3044

Random effects:

Groups Name	Variance	Std.Dev.
dyad (Intercept)	0	0

Number of obs: 109, groups: dyad, 3

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.533775	1.844657	0.831	0.4057
abs_numfemales	-0.258008	0.208794	-1.236	0.2166
abs_infants	0.137551	0.163839	0.840	0.4012
abs_numswfem	-0.030153	0.115223	-0.262	0.7936
abs_UD190	-0.001968	0.012798	-0.154	0.8778
durationIGE	0.030217	0.010409	2.903	0.0037 **

```

---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) abs_nmf abs_nf abs_nms a_UD19
abs_numfmls  -0.868
abs_infants  -0.050 -0.210
abs_numswfm  -0.145 -0.152  0.276
abs_UD190    -0.151 -0.001 -0.002 -0.107
durationIGE  -0.352  0.121 -0.067 -0.102 -0.017
>
> cat("\n\n Comparison of female-based (full; DC) model to null model\n\n")

```

Comparison of female-based (full; DC) model to null model

```

>
> print(anova(res.null,res_new, test="Chisq"))
Data: data
Models:
res.null: aggression_yn ~ durationIGE + (1 | dyad)
res_new: aggression_yn ~ abs_numfemales + abs_infants + abs_numswfem +
res_new: abs_UD190 + durationIGE + (1 | dyad)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
res.null 3 79.328 87.402 -36.664  73.328
res_new  7 84.625 103.464 -35.312  70.625 2.7032      4      0.6087
>
> #AIC values to the list
> models[[3]]<-res_new
> Modnames <- rbind(Modnames, "Model with new variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_new<-r.squaredGLMM(res_new)
The result is correct only if all data used by the model has not changed since model was fitted.
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model failed to converge with max|grad| = 0.00163829 (tol = 0.001, component 1)
> R2<-rbind(R2,r2_new)
>
>
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_numfemales", geom.colors = "bw",show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model()` instead.
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_infants",geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :

```

```

the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_numswfem",ge
om.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="durationIGE",geo
m.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
>
>
> #####
#####
> #####
#####
> #####
#####
> cat("\n\n\n RESULTS \n\n\n")

```

RESULTS

```
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = N
ULL, sort = TRUE)
```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcwt	Cum.Wt	LL
null model	3	79.56	0.00	0.93	0.93	-36.66
Model with new variables	7	85.73	6.18	0.04	0.97	-35.31
Model with original variables	7	86.32	6.76	0.03	1.00	-35.61

Warning message:

```

In data.row.names(row.names, row si, i) :
some row.names duplicated: 3 --> row.names NOT used
> R2

```

	R2m	R2c
R2	0.7839939	0.7839939
r2_original	0.7793538	0.7793538
r2_new	0.7705370	0.7705370

```
> cat("\n\n\n\n\n\n\n  Non-Contact/Contact AGGRESSION \n\n\n\n\n\n\n")
```

Non-Contact/Contact AGGRESSION

```
>
> ## Upload data
> data<-read.csv("Data_for_revision_subsample.csv")
>
>
>
>
>
> ###Convert variables to the appropriate format
> data$num_obs<- as.numeric(data$num_obs)
> data$dyad<- factor(data$dyad)
> data$durationIGE<- as.numeric(data$durationIGE)
> data$abs_numfemales<- as.numeric(data$abs_numfemales)
> data$abs_infants<- as.numeric(data$abs_infants)
> data$abs_numinfperfem<- as.numeric(data$abs_numinfperfem)
> data$abs_numswfem<- as.numeric(data$abs_numswfem)
> data$abs_swfemperfem<- as.numeric(data$abs_swfemperfem)
> data$abs_UD190<- as.numeric(data$abs_UD190)
> data$decided_undecided<- as.factor(data$decided_undecided)
> data$aggression_yn<- as.factor(data$aggression_yn)
> data$aggression_level<- as.factor(data$aggression_level)
>
> #Eliminating NAs (otherwise when calculating the null models the sample
size is different and the comparison cannot be made)
> missingrows = is.na(data$abs_numfemales)
> data= data[!missingrows,]
> missingrows = is.na(data$abs_numinfperfem)
> data= data[!missingrows,]
> missingrows = is.na(data$abs_swfemperfem)
> data= data[!missingrows,]
> missingrows = is.na(data$aggression_level)
> data= data[!missingrows,]
>
>
> cat("\n\n Null model \n\n")
```

Null model

```
>
> res.null=glmer(aggression_level ~ durationIGE+ (1|dyad), family="binomi
al", data=data)
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?
>
```

```

> #AIC values to the list
> models<-list()
> models[[1]]<-res.null
> Modnames <- "null model"
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_null<-r.squaredGLMM(res.null)
The result is correct only if all data used by the model has not changed since model was fitted.
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
> R2<-r2_null
>
>
> cat("\n\n\n\n\n\n\n\n Using original variables (Proportions of tumescent females and infants per female) \n\n\n\n\n\n\n\n\n")

```

Using original variables (Proportions of tumescent females and infants per female)

```

>
>
> #Checking co-linearity (Values close to 1 are good, over 4 can be problematic)
> vif(glm(aggression_level ~ abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_UD190+durationIGE, family="binomial", data=data))
      abs_numfemales abs_numinfperfem abs_swfemperfem      abs_UD190      durationIGE
1.031987      1.120549      1.099008      1.044108
1.068846
>
> #Run the model
> res_original=glmer(aggression_level ~ abs_numfemales+abs_numinfperfem+abs_swfemperfem+abs_UD190+durationIGE+(1|dyad), family="binomial", data=data)
Warning messages:
1: Some predictor variables are on very different scales: consider rescaling
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue

```

```

- Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
>
> print(summary(res_original))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: aggression_level ~ abs_numfemales + abs_numinfperfem + abs_swfemp
erfem + abs_UD190 + durationIGE + (1 | dyad)
Data: data

      AIC      BIC    logLik deviance df.resid
    114.4    132.1    -50.2    100.4      85

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.9480 -0.6472 -0.4297  0.7427  2.5865

Random effects:
Groups Name      Variance Std.Dev.
dyad    (Intercept) 0        0
Number of obs: 92, groups: dyad, 3

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)    0.502530   1.174277   0.428   0.6687
abs_numfemales -0.286298   0.138211  -2.071   0.0383 *
abs_numinfperfem 2.320974   2.558923   0.907   0.3644
abs_swfemp erfem -0.526961   2.792110  -0.189   0.8503
abs_UD190      -0.010339   0.009857  -1.049   0.2942
durationIGE      0.004807   0.002177   2.208   0.0272 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) abs_nmf abs_nmn abs_sw a_UD19
abs_numfmls  -0.830
abs_nmnfprf  -0.300  0.038
abs_swfmp rf  -0.155 -0.077 -0.253
abs_UD190     -0.247  0.128 -0.075 -0.115
durationIGE   -0.110 -0.117 -0.208  0.139 -0.057
fit warnings:
Some predictor variables are on very different scales: consider rescaling
convergence code: 0
Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?
Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?

>
> cat("\n\n Comparison of model with original variables and model to null
1 model\n\n")

```

Comparison of model with original variables and model to null model

```

>
> print(anova(res.null,res_original, test="Chisq"))

```



```

Data: data
Models:
res.null: aggression_level ~ durationIGE + (1 | dyad)
res_original: aggression_level ~ abs_numfemales + abs_numinfperfem + abs_s
wfemperfem +
res_original: abs_UD190 + durationIGE + (1 | dyad)

```

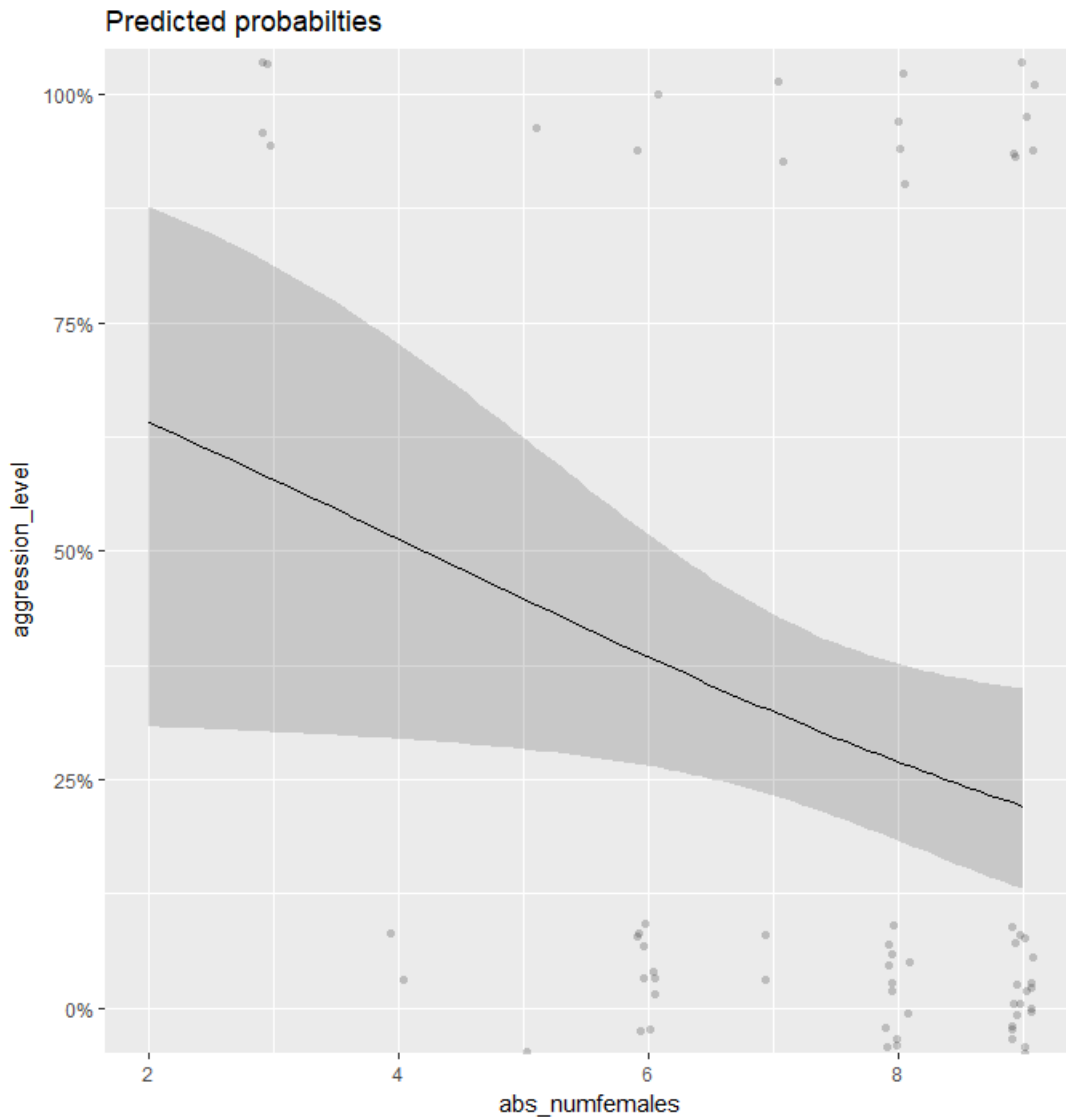
	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
res.null	3	112.73	120.3	-53.368	106.73				
res_original	7	114.45	132.1	-50.223	100.45	6.2896		4	0.1785

```

>
> #AIC values to the list
> models[[2]]<-res_original
> Modnames <- rbind(Modnames, "Model with original variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_original<-r.squaredGLMM(res_original)
The result is correct only if all data used by the model has not changed since model was fitted.
Warning messages:
1: Some predictor variables are on very different scales: consider rescaling
2: In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
  - Rescale variables?;Model is nearly unidentifiable: large eigenvalue ratio
  - Rescale variables?
> R2<-rbind(R2,r2_original)
>
>
>
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_numfemales",geom.colors = "bw",show.ci=TRUE)
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :

```

the matrix is either rank-deficient or indefinite

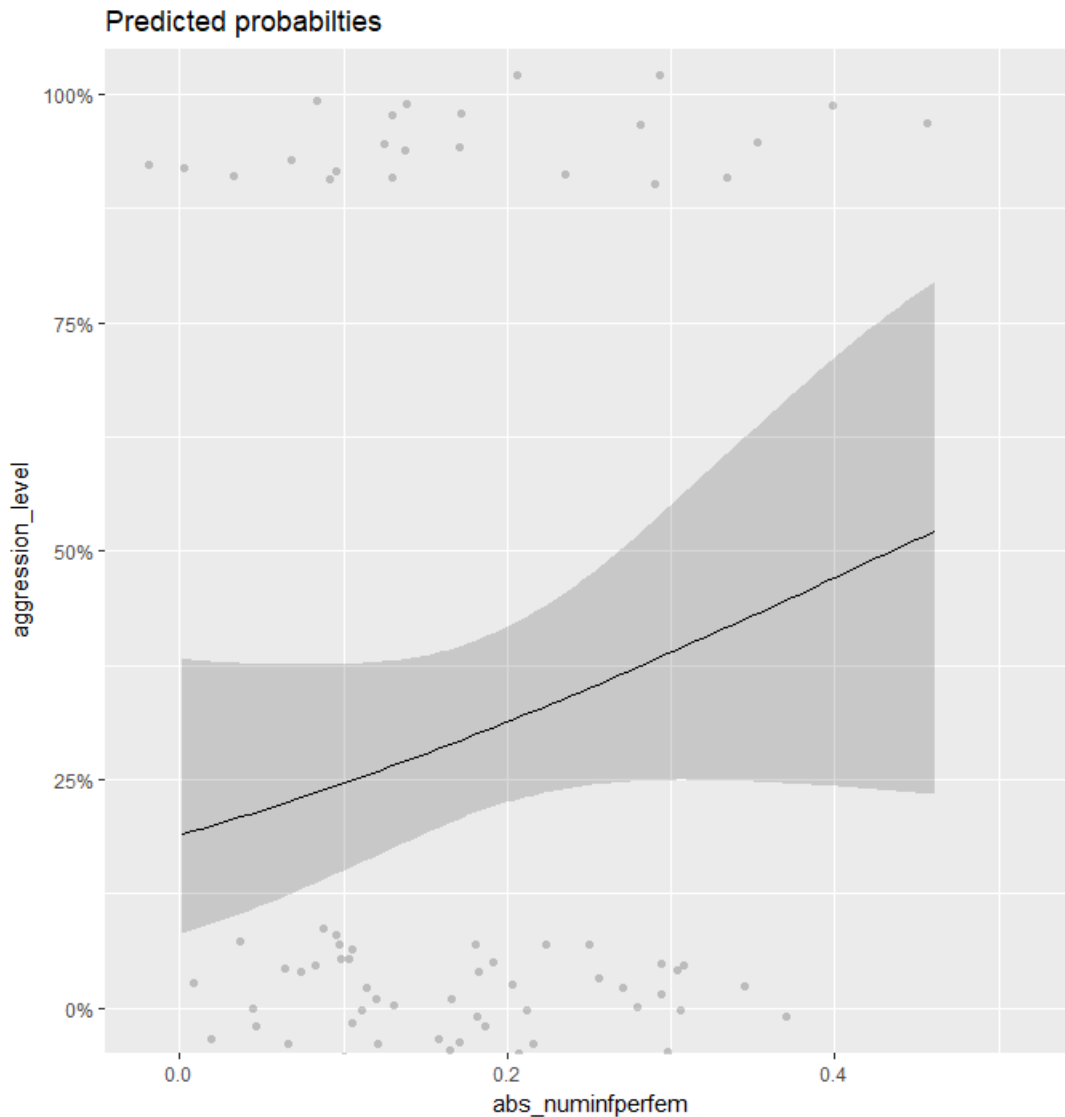


```
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_numinfp
erfem",geom.colors = "bw",show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model
()` instead.
```

warning messages:

```
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
```

the matrix is either rank-deficient or indefinite



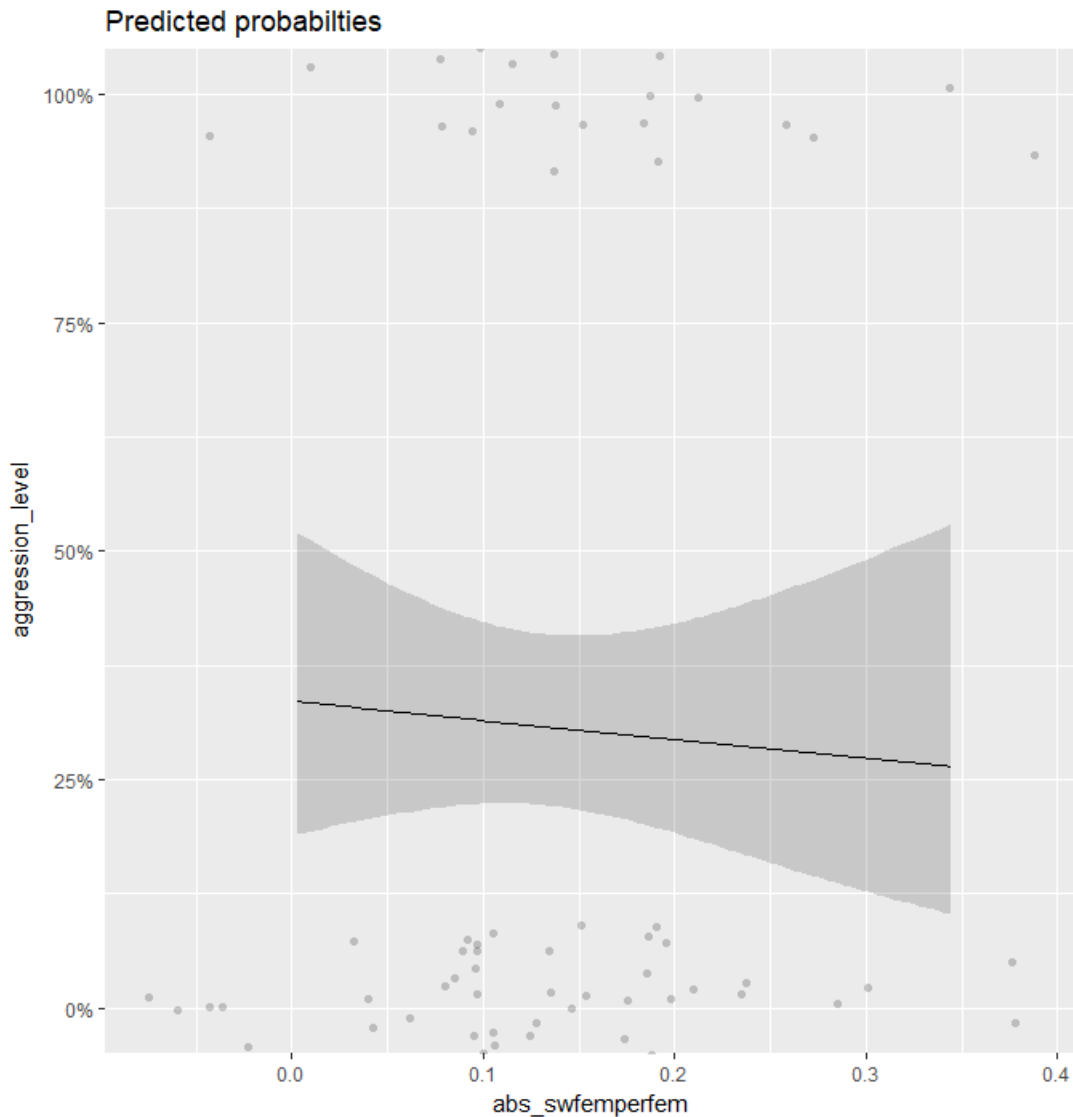
```
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="abs_swfempe  
rfem",geom.colors = "bw",show.ci=TRUE)
```

``sjp.glmer()` will become deprecated in the future. Please use `plot_model`
()` instead.`

warning messages:

- 1: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 2: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 3: In chol.default(sigma, pivot = TRUE) :

the matrix is either rank-deficient or indefinite

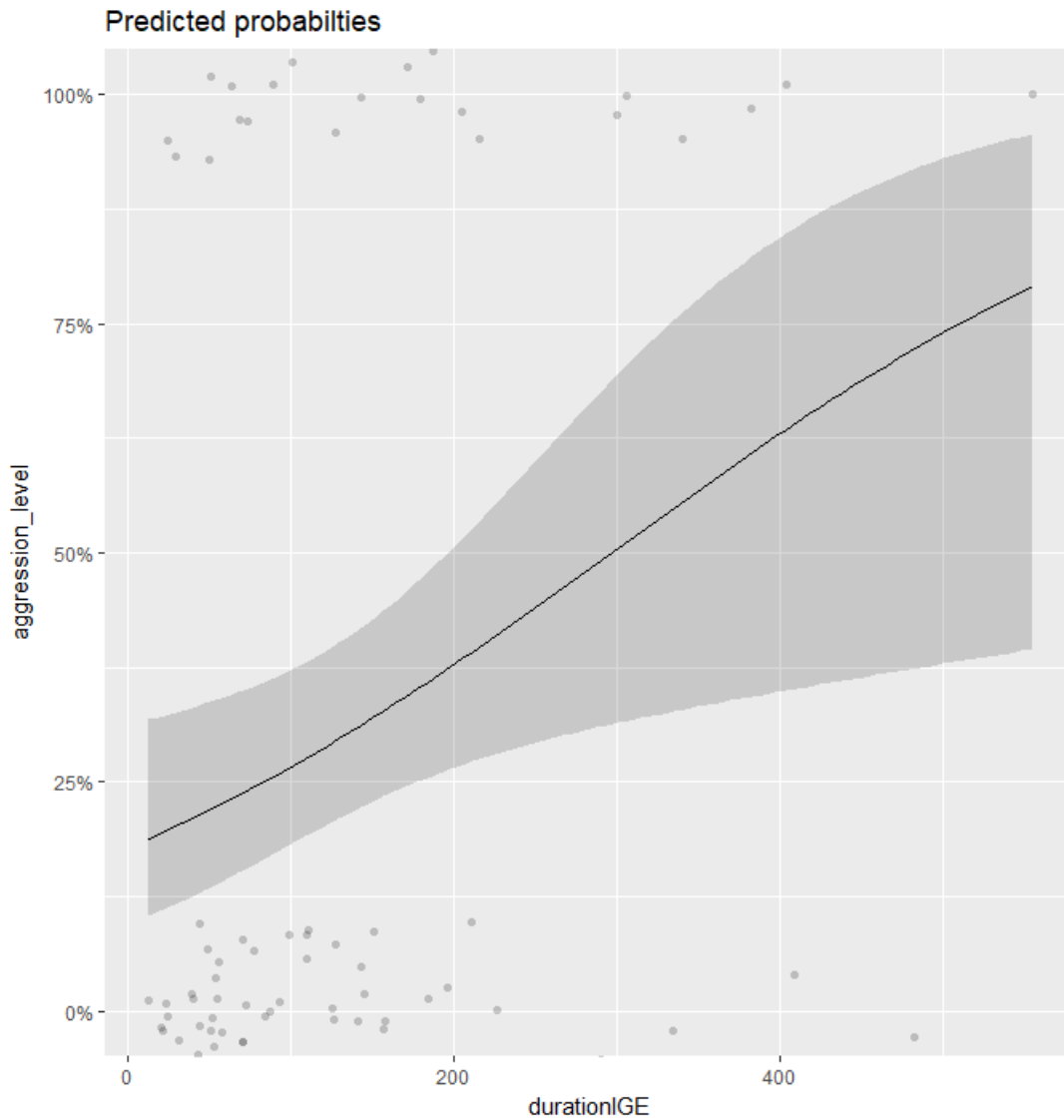


```
> sjp.glmer(res_original, type="pred", facet.grid=FALSE, vars="durationIGE",
  ",geom.colors = "bw",show.ci=TRUE)
```

Warning messages:

- 1: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 2: In chol.default(sigma, pivot = TRUE) :
the matrix is either rank-deficient or indefinite
- 3: In chol.default(sigma, pivot = TRUE) :

the matrix is either rank-deficient or indefinite



```
>
>
>
> cat("\n\n\n\n\n\n\n\n Variables proposed in viva (No.infants/Females with
infants and No. tumescent females) \n\n\n\n\n\n\n\n\n")
```

Variables proposed in viva (No.infants/Females with infants and No. tumescent females)

```

>
> #Checking co-linearity (values close to 1 are good, over 4 can be problematic)
> vif(glm(aggression_level ~ abs_numfemales+abs_infants+abs_numswfem+abs_UD190+durationIGE, family="binomial", data=data))
abs_numfemales    abs_infants    abs_numswfem    abs_UD190    durationIGE
          1.068555          1.078715          1.085576          1.050172          1.043776

>
> #Run the model
> res_new=glmer(aggression_level ~
+               abs_numfemales+abs_infants+abs_numswfem+abs_UD190+durationIGE+
+               (1|dyad), family="binomial", data=data)
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?
>
> print(summary(res_new))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: aggression_level ~ abs_numfemales + abs_infants + abs_numswfem + abs_UD190 + durationIGE + (1 | dyad)
Data: data

            AIC      BIC    logLik deviance df.resid
        114.8    132.4    -50.4    100.8      85

Scaled residuals:
      Min       1Q   Median       3Q      Max
-2.1448 -0.6339 -0.4391  0.7614  2.5683

Random effects:
Groups Name      Variance Std.Dev.
dyad   (Intercept) 0        0
Number of obs: 92, groups: dyad, 3

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   0.663198   1.139274   0.582   0.5605
abs_numfemales -0.306116   0.139889  -2.188   0.0286 *
abs_infants    0.078928   0.114298   0.691   0.4898
abs_numswfem   0.016478   0.096092   0.171   0.8638
abs_UD190     -0.010272   0.009967  -1.031   0.3027
durationIGE    0.005447   0.002157   2.525   0.0116 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) abs_nmf abs_nf abs_nms a_UD19
abs_numfm1s  -0.791
abs_infants  -0.202 -0.159
abs_numswfm  -0.263 -0.143  0.212
abs_UD190    -0.271  0.157 -0.075 -0.161
durationIGE  -0.206 -0.135  0.143  0.117 -0.090
convergence code: 0

```

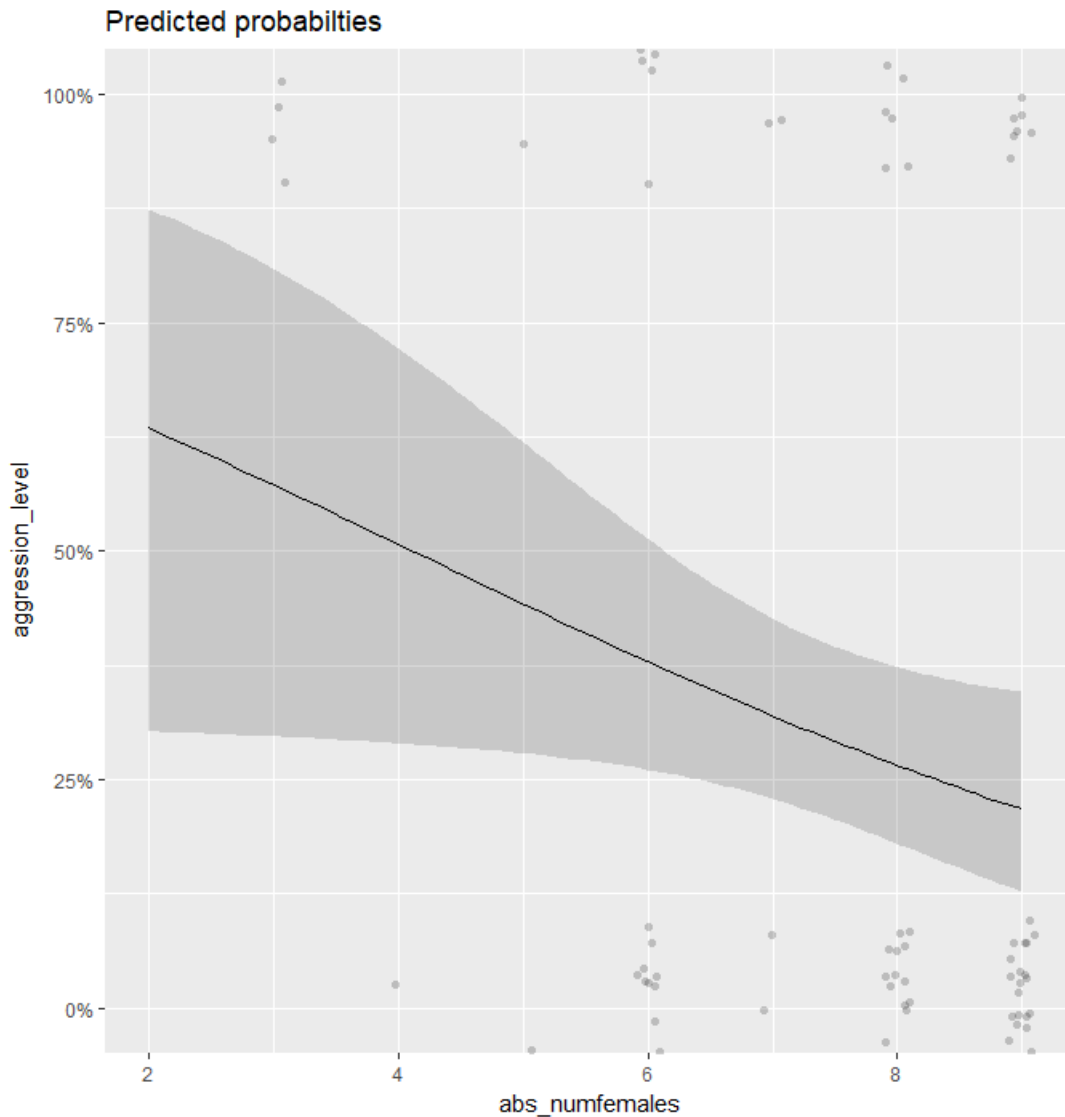
Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?

```
>
> cat("\n\n Comparison of female-based (new) model to null model\n\n")
```

Comparison of female-based (new) model to null model

```
>
> print(anova(res.null, res_new, test="Chisq"))
Data: data
Models:
res.null: aggression_level ~ durationIGE + (1 | dyad)
res_new: aggression_level ~ abs_numfemales + abs_infants + abs_numswfem +
res_new: abs_UD190 + durationIGE + (1 | dyad)
      Df    AIC    BIC logLik deviance Chisq Chi Df Pr(>Chisq)
res.null  3 112.73 120.30 -53.368   106.73
res_new   7 114.79 132.44 -50.394   100.79 5.9464     4    0.2032
>
> #AIC values to the list
> models[[3]]<-res_new
> Modnames <- rbind(Modnames, "Model with new variables")
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and Schielzeth, 2013)
> r2_new<-r.squaredGLMM(res_new)
The result is correct only if all data used by the model has not changed since model was fitted.
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: very large eigenvalue
- Rescale variables?; Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
> R2<-rbind(R2, r2_new)
>
>
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_numfemales",
geom.colors = "bw", show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model()` instead.
Warning messages:
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
```

the matrix is either rank-deficient or indefinite

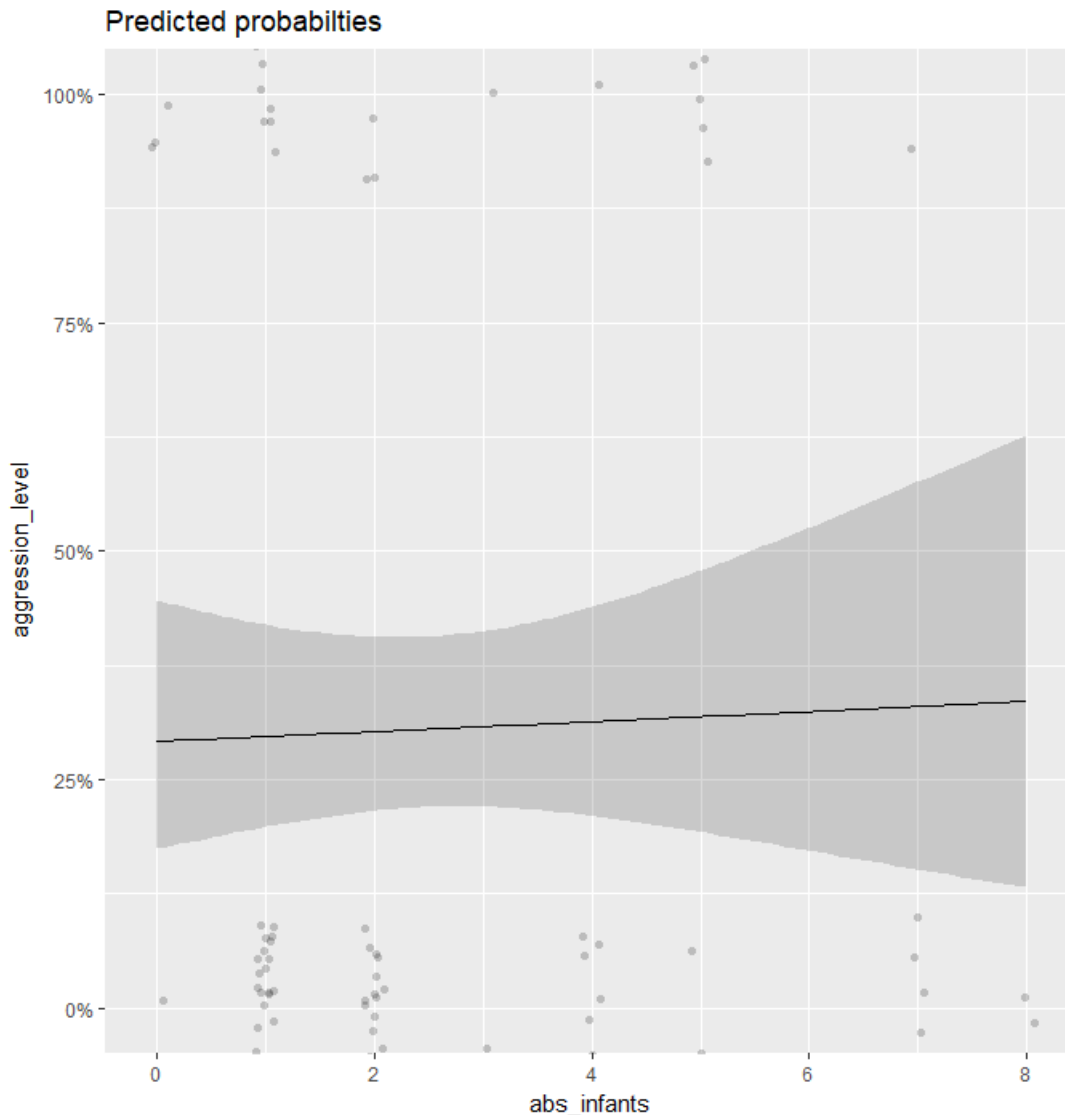


```
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_infants", geo
m.colors = "bw", show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model
()` instead.
```

warning messages:

```
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
```


the matrix is either rank-deficient or indefinite

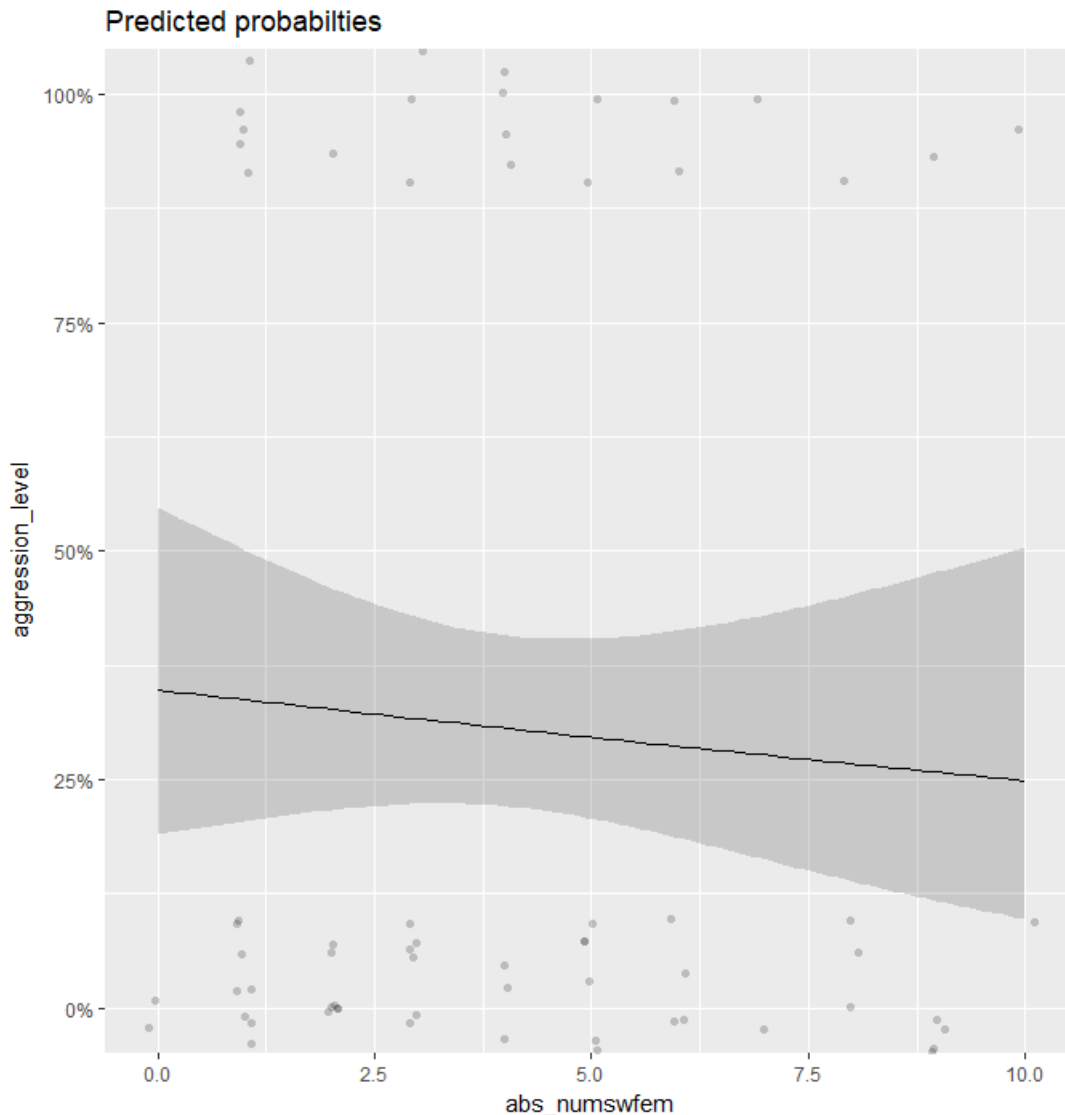


```
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="abs_numswfem", geom.colors = "bw", show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model()` instead.
```

warning messages:

```
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
```

the matrix is either rank-deficient or indefinite

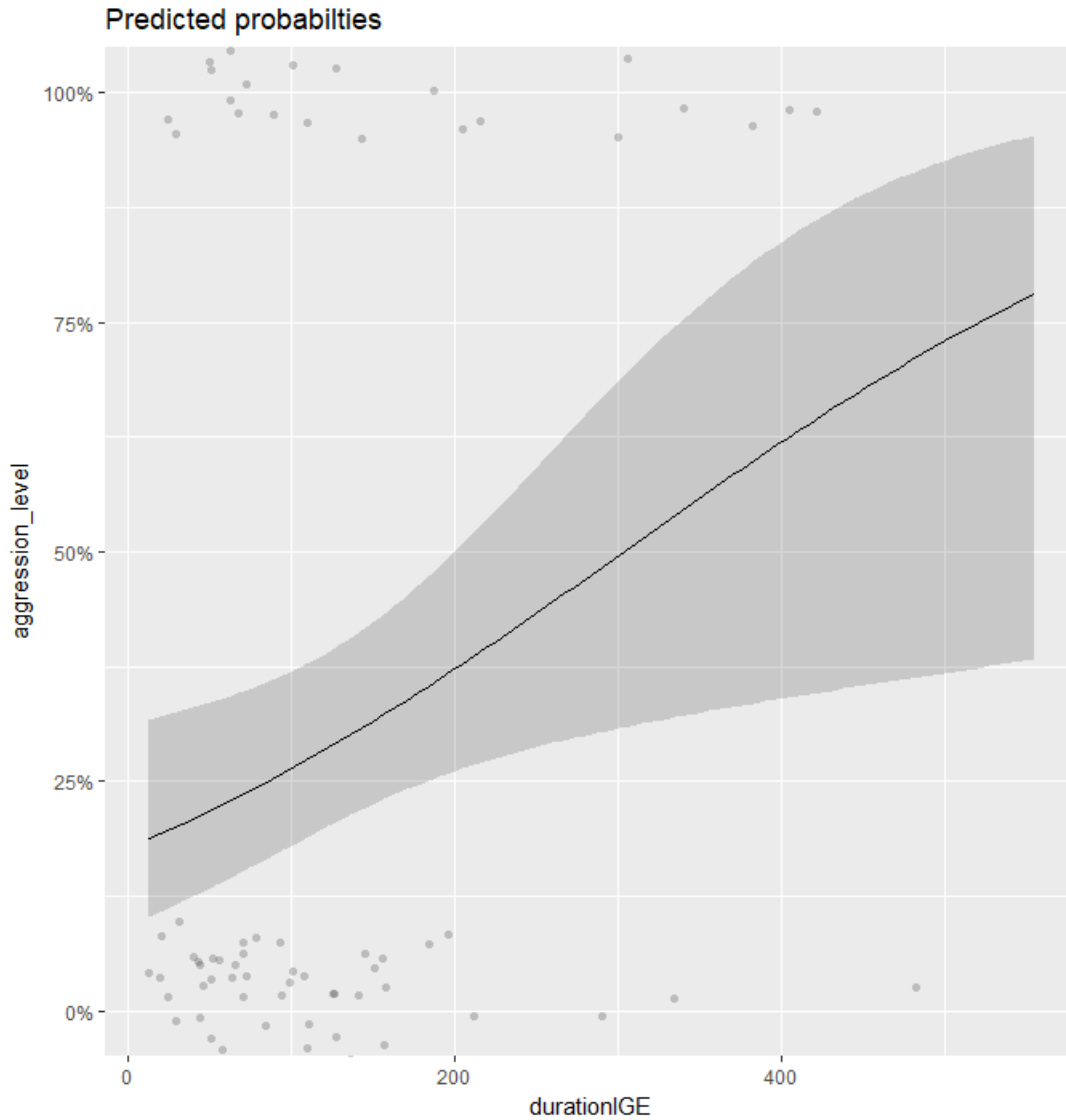


```
> sjp.glmer(res_new, type="pred", facet.grid=FALSE, vars="durationIGE", geom.colors = "bw", show.ci=TRUE)
`sjp.glmer()` will become deprecated in the future. Please use `plot_model()` instead.
```

warning messages:

```
1: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
2: In chol.default(sigma, pivot = TRUE) :
  the matrix is either rank-deficient or indefinite
3: In chol.default(sigma, pivot = TRUE) :
```

the matrix is either rank-deficient or indefinite



```
>
>
> #####
> #####
> #####
> #####
> cat("\n\n RESULTS \n\n")
```

RESULTS

```
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs = N
ULL, sort = TRUE)
```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcwt	Cum.Wt	LL
null model	3	113.01	0.00	0.68	0.68	-53.37

```

Model with original variables 7 115.78      2.77    0.17    0.86 -50.22
Model with new variables      7 116.12      3.11    0.14    1.00 -50.39

```

```

warning message:

```

```

In data.row.names(row.names, rowsi, i) :
  some row.names duplicated: 3 --> row.names NOT used

```

```

> R2

```

```

              R2m      R2c
R2           0.08730261 0.08730261
r2_original  0.18162395 0.18162395
r2_new       0.17805568 0.17805568

```

Female-based models with integer and ratio variables are equivalent in the trends shown, AICc and R^2 when using absolute values of the variables

CHAPTER 4: SUPPLEMENTARY INFORMATION

4.1. Narration of the intergroup coalitionary aggressions recorded between November 2015 and July 2016

18TH DECEMBER 2015: LETHAL ATTACK ON A FEMALE BY PB1 MEMBER

Summary

Observer/s: LI, RY

Victim: Adult female of unhabituated group

Aggressor group: PB1

I was following PB1 with 4 other observers (RY, ML, MS, IW) and I was looking for my next focal. The group was very spread out and I lost contact of the monkeys for some minutes. When I finally found some of them again (10:48), they were already attacking the female. A juvenile male¹, called Sashimi, and an adolescent female, Emping, were the two individuals more involved in the aggression. They both bit her repeatedly and through the whole observation. Some unidentified juveniles also bit the victim, whenever the other two allowed it. An adult female, Jane, was seen biting the unknown female only twice. While Emping and the juveniles focused their bites on the female's limbs, Sashimi did so on her throat. Possibly, one of those bites killed the female by suffocating her. There was one in particular, at 10:54:45, that lasted for 15 seconds, that seems the most likely candidate. Before this bite, the female did not struggle and

¹ Sashimi was almost a sub-adult. He was bigger than a female but he still lacked other features to categorize him as sub-adult. Those were elongated canines and reddish skin on the anal area.

played death most of the time, although it was possible to see some limb movement every now and then. The most obvious movement occurred at 10:52:50, when she turned herself upside down. After the bite mentioned above, no more movements were detected, but a swallow breath was detected by the observer the day of the recording. Nonetheless, this is not appreciated on the video.

Besides bites, some attacks consisted on pulling parts of the victim's body and dragging her. These were a minority in comparison to the bites and occurred mostly after the presumed death.

Many bystanders examined the body, sometimes touching briefly and/or sniffing. There were periods in which nobody interacted with the victim and the monkeys around continued normal activities.

There were 2 moments in which the victim was left alone. The first one occurred at 10:59, when the victim is left for 1 minute and a half, after Kristi, one of the adult females had been examining her. Interestingly, she comes back vocalizing softly, followed by Sashimi, who bites the female on the abdomen while Kristi vocalizes excited and Emping appears running and joys the new bout of attacks, together with a couple of juveniles. Around 11:15 is again left on her own for a bit more than a minutes, when Sashimi and Emping. She is left on her own once again, Sashimi comes into visual contact but leaves definitively afterwards.

Examination of the body showed superficial injuries on her right arm (2-3cm), 2 on the groin (~3cm each), several lacerations of about 1cm each on the chest and one on the throat of ~1.5 cm. None of them bleed, and seemed to only pierce the skin. If the cause of death was the attack, which seems likely, I would presume was due to suffocation due to the bites directed to her throat.



Figure I Snapshots of the attack by PB1 on an unknown female the 18th December 2015. AF= Adolescent female (In this case always Emping); F= Adult Female (In this case always JP and BC); j=Juveniles J=Juvenile (Sashimi); V=Victim

Full description

It was 18th December 2015 at 10:48. I was following PB1 with 4 other observers (RY, ML, MS, IW) and I was looking for my next focal. The monkeys were very spread out and I lost contact of any of them for some time. When I finally found some more monkeys, they were already attacking the female (UF=Unknown Female) and I started recording the event by 10:49.

At that point, within 2 meters of the victim, there were 2 juveniles 2 individuals that couldn't be identified, 2 adult females (Jane and Bianca), Emping (AF) and Sashimi (J). BLS=Body lengths (average female body-length from shoulders to beginning of the tail).

Sashimi and Emping bite the female violently. The female does not struggle, but moves her hind legs slightly. Meanwhile, Bianca displaces juveniles around the victim, while Sashimi and Emping keep biting her at intervals (Figure I, Picture 1). A juvenile approaches but is displaced by Bianca. Emping hugs Bianca and she reciprocates. By now, only BP, Sashimi, Emping, SP and a juvenile are within 2 m of the female. A minute later, Sashimi leaves and two juveniles touch the female, pulling her arms and nipples. She does not respond. Sashimi grabs the left arm of the victim and pulls towards him. The female faces upwards with open eyes and grinning, looking dead. Emping bites the female. Sashimi leaves and once the female is stopped of being attacked, she turns around, lying on her stomach. Later on, Sashimi bites the victim on the throat, Emping bites different parts at intervals.

Sashimi, who had left the scene, gets closer to the female, bends and bites strongly her left flank while holding her head with his left arm, turns her around and steps on her head with his left foot. A juvenile and Emping pull from the female in different directions while Sashimi attacks her. Jane approaches, smells the female and sits. Emping moves towards the female's face and then bites her and pulls her hair while Sashimi keeps biting as well.

Emping bites UF's left leg, Sashimi touches UF's head. And UF seems to try to stand up, moving her hind legs. Emping pushes her down with her left arm while still biting her. JP seems to join and so does Sashimi, grabbing UF's head (Figure I, Picture 2). When they stop, Sashimi turns the female around, so the ventral part faces upwards. The Sashimi bites her again between the chest and the throat. Then he sits down while UF faces upwards with open eyes and a grin. We see a juvenile, JP, BP, Emping and Sashimi surrounding her. Then Sashimi grabs UF's lips and pulls them open before bending and smelling the mouth. JP and BP leave and Emping grooms UF slightly, then she bites her.

Sashimi grabs UF's right arm and pulls. Then he bends towards her and, while putting his left hand over her eyes, seems to bite her on the back of her neck and then the throat (Figure I, Picture 3). Emping and a juvenile are touching her meanwhile. Sashimi stops biting UF's throat. The juvenile bites her and Emping is in body contact with her. Another juvenile grabs her left arm and pull from her, displacing her. Then it leaves.

Emping bites again and JP and BP appear in scene. 2 juveniles are seen as bystanders too. Emping drags UF while biting her. Sashimi and a juvenile follow. Emping stops biting and a juvenile and Sashimi do. BP displaces a juvenile. A juvenile and Sashimi bite again UF, with Emping in close proximity, but obscured by Sashimi. Another juvenile approaches UF, grabs her head, pulls softly and grooms. The other juvenile bites around UF's groin. Sashimi grabs UF's left leg, pulls and smells the foot.

A juvenile pulls UF towards it grabbing a leg and the drags. Another juvenile jumps around and a third one approaches to the head (not seen what it does). One of the juveniles bites the right flank and is then displaced by Emping, who ignores it is lip-smack and approaches UF. UF lies facing upwards with a grin.

Emping bends and smells UF's mouth. A juvenile touches UF's right thigh. Emping displaces it and bites that area. Then a juvenile passes its hands over the area. Emping pulls UF's right nipple. BP and JP are in the scene (Figure I, Picture 4). BP is grooming the juvenile that grooms UF. The juvenile stops grooming UF. JP leaves the scene. BP stops grooming juvenile. Emping touches UF with both hands. Juvenile grooms UF. Juvenile turns UF around. Another juvenile touches and Emping examines UF's groin. UF is left resting on her right flank.

Sashimi bends and examines the head. Then he bites the throat strongly. BP leaves the scene and a juvenile grooms UF's hindquarters. Sashimi leaves the scene running and a juvenile follows. Then Emping moves away from UF. A juvenile then bends towards UF's hindquarters and examines

We hear vocalizations typical of a conflict and Emping runs away from scene. The 2 juveniles close to Emping look toward the direction Emping ran to. There is another individual over 5bls away, on the background.

The juvenile who was in body contact with UF runs away from scene. The juvenile who was on the background comes closer (2-3bls). Then it and the juvenile who was close to UF run away from scene. No monkey is seen around UF. UF lies on her right flank, she seems to breath. A juvenile appears in scene and approaches. Looks around and bends to "smell" The juvenile seems to touch UF (but then the camera moves and cannot see). Then "smells" again and looks around. The juvenile touches UF, smells and moves around. The juvenile lip-smacks to someone out of scene and moves away from UF (1-2 bls). KP appears and approaches UF.

KP bends and seems to smell UF, but her body covers what she does. The juvenile approaches her teeth-chattering She lips-smacks. Then she continues examining UF, the juvenile sits and grooms UF briefly.

KP “smells” the head of UF. The juvenile smells the left foot. KP is sitting close to UF’s head. Juvenile (I think is GA...?) greets someone, I don’t know if to KP or someone out of the scene. The juvenile grooms UF’s hindquarters for a couple of seconds The juvenile lip-smacks at KP and KP lip-smacks back. Then the juvenile approaches KP and smells UF head area. The juvenile grooms UF and KP stands up and leaves the scene. The juvenile follows. The move the camera around and I can only locate KP and the juvenile moving away. No more monkeys visible in the proximity.

A monkey starts approaching from over 5 meters away. Is KP again. Vocalizes. A juvenile and Sashimi also approach. I retreat, moving away from UF. Sashimi approaches UF and bites her belly. KP approaches vocalizing Emping approaches UF, Sashimi and KP running. Sashimi “smells” hindquarters and Emping examines the head and bites. Another juvenile next to her examines, and seems to bite the belly too. A second juvenile approaches displacing the first one. Sashimi bites the head area, obscuring Emping. Both, Emping and Sashimi bite around the head, while the juvenile that just approached “smells” the anal area of UF. Another juvenile approaches and touches UF’s right arm and then bites. Another juvenile appears in the scene.

The juvenile who just appeared in the scene gets close to UF. Sashimi is sitting on UF’s body. Emping MOVES away (but still within 0’1bls) and Sashimi bites UF again around the head-neck area. Emping bites UF Around THE left arm and a juvenile seems to bite UF around the head too, but Sashimi and Emping are in front, so is not clear. Emping stands up while biting UF, pulling her arm up with her mouth, while pushing the body against the ground with her right arm. The juvenile that was close to Emping jumps away when she looks at it. Emping smells UF’s anal area and sits in body contact. Sashimi stops biting UF, the juvenile that appeared biting before is no longer close to UF and KP is not in scene. Sashimi leaves UF, KP is seen in scene vocalizing towards UF, Emping stands up in to legs and looks away, towards the direction Sashimi is heading. Then she runs that way and KP looks towards that direction. Then KP looks at UF and sits within 2bls of her.

Two juveniles that were within 3m of UF leave, only KP remains visible in proximity. Sashimi approaches again and KP vocalizes. Sashimi bends and bites UF around the left armpit. Sashimi stops biting and smells the anal area. KP keeps vocalizing. Emping comes back and touches UF’s head, then grabs her face and pulls her head briefly upwards. A juvenile approaches and sits 1-2 bls away of UF. Emping leaves. KP leaves. A juvenile approaches UF. Sashimi is in body contact with her. Then he stands up in two legs and looks away before sitting again. The juvenile smells UF. Sashimi moves towards UF displacing the juvenile. Then he bites the left flank while the juvenile vocalizes. Afterwards Sashimi tries to turn UF around (she is facing the ground at this point). Sashimi puts UF’s body on the left flank and grooms the belly for a moment.

Sashimi runs away and disappears from scene. Then the juvenile starts leaving, stopping briefly to observe UF. A juvenile approaches UF, look at her and grooms the belly briefly, then turns around the body and grooms the back briefly. Loud call. The juvenile touches UF slightly and another juvenile appears within 3 bls. Emping runs towards UF displacing the 2 juveniles that were close to her. She stops almost in body contact with her. Then Sashimi approaches too. Emping seems to bite slightly on the lower belly (not clear). A juvenile approaches. Emping bites UF belly Emping moves a bit away: Sashimi starts following her, grabs UF left arm and drags her with him towards Emping (Figure 1, Picture 5). Then the 3 of them (Sashimi, Emping and the juvenile) examine UF, smelling and touching. Emping bites the right arm. Sashimi pulls the head up. Looks the face closely and seems to lip smack before biting the throat. The juvenile jumps away and Emping bites the lower belly. The juvenile approaches again, grabs UF left leg and pulls towards him while Sashimi and Emping bite UF. A juvenile comes running towards them. The juvenile that was already there is also biting now. Emping leaves.

Sashimi grabs the right arm and pulls. Then he moves away and stays within 3bls and a juveniles smells UF breast. The other juveniles approaches, smells and grooms slightly. One of the juveniles leave, the other grooms a bit and then examines the anal area. The juvenile grooms UF again. The juvenile grabs UF's left leg and smells her groin. Then grooms the belly slightly. Another juveniles approaches and stays close for 20 seconds. UF is not seen breathing any more. I don't know when she stopped. Sashimi is groomed by a juvenile within 5bls of UF. A juvenile is around the UF's body examining it. Then it bites it (00:06) and grooms it. Then, after manipulating the body with its hands, sits, apparently in body contact and waits. The juvenile grooms UF's body briefly again. The sits on the other side of it. Vocalizations are heard and the juvenile leaves UF (maybe displaced by Sashimi? Inferred). Sashimi approaches UF again and bites her breast and then the throat. The juvenile looks from 4-5bls. Sashimi bites UF's right nipple repeatedly and pulls. Sashimi turns the body around, examines the anal area and then pulls the body towards him, so UF's anal area is pointing upwards and her head and arms lie on the ground. Then he bites the groin. The juvenile approaches and after few seconds bites the throat area while Sashimi bites tights and belly. Then the juvenile bites also the belly-tight area. Sashimi bites the throat and the juveniles the groin area. Sashimi grabs the right arm and drags the body about 1bls. Then he bites the throat and the juveniles approaches the body again. There is another monkey about 3-4bls away. Sashimi pulls from one of UF's nipples. Then stands up and "kicks" the body with his left leg. Then he moves away a couple of bls. The monkey that was looking from 3-4bls is a juvenile male. The juvenile close to the body bites the tights. The juvenile moves away from the body (vocalizations are heard on the background). Sashimi also moves away from the scene. The other juvenile approaches the body and examines before moving away at 04:00

Emping and Sashimi start approaching to UF again. By 5:26 Sashimi is there biting her again on the belly-groin area with Emping by his side, who bites the left armpit area, while Sashimi moves to bite the chest. Sashimi starts walking away and Emping follows after smelling UF's body once more. They Sit within

4-5 bls of UF. There is a zoom in to Sashimi face and when the camera zooms out at 6:14, Emping is gone. Sashimi stays within 5 bls self-grooming and looking around. Sashimi approaches UF body again and grooms her chest and shoulders (Figure I, Picture 6). Sashimi leaves UF's body. End of the second video. No monkey seen around the body.

At the beginning of the third video, a monkey approaches from far and looks towards the body from 5-10 bls. The monkey approaches UF's body. He is Sashimi again. Looks at the body and leaves (01:28).

No more monkeys approached the body after this. We examined the body looking for injuries (there is a video of it) and wait until Iwan and Meidy arrived to take the body to camp. There the body was measured by Meldy, Meidy, Andre, etc, a genetic sample was taken and then was buried under the stairs of POS3.

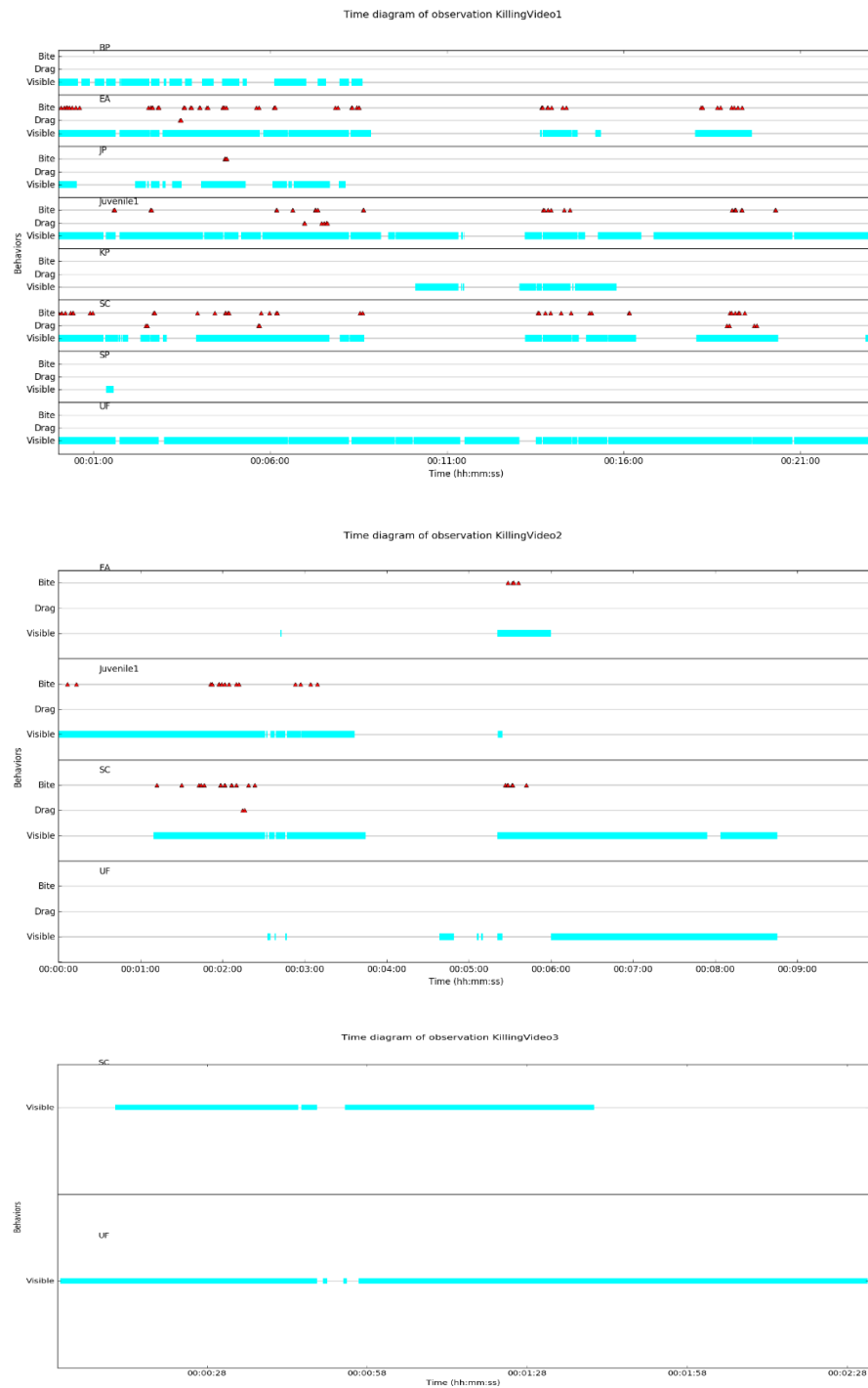


Figure II Time-diagrams of the attack on unknown female by PB1 (18th December 2015).

20TH FEBRUARY 2016 CASE: R2 FEMALE JUVENILE TRAPPED BY R1*Summary***Observer/s:** LI, JB (JM, MS, SJ, TS)**Victim:** Juvenile female from R2**Aggressor group:** R1

During an encounter between R1 and R2, a juvenile (most likely a female according to what can be seen in the recording) was trapped by R1 between the buttresses of a tree. When the encounter finished I started to cover the event. Due to the location where the victim was, many of the attacks could not be seen accurately, since they were obscured by the buttresses and/or the monkeys sitting on them.

It was obvious however that at least XK, 2 unidentified adolescent females and several juveniles bit the victim and manipulated the body, pulling limbs and pushing the victim, who remained passive most of the time, playing death. The victim only moved occasionally, to lip-smack at the monkeys around her and to turn herself down. Two of the attacks had good visibility. Both were carried out by juvenile males. In one, the juvenile bit the upper part of the victim and pulled her upwards until she was standing before releasing the bite. The other was directed to the throat. From the 48 individuals that could be individually identified at the time in R1, 25 came within one meter of the victim during the recording and observed. This included 5 males, 2 of them (TM and AK) directed a short look to it and continued their activities. The other 3 (BM, EJ and SN) looked at the victim a bit more and stayed within proximity, but none of them went inside the gap to interact with it. Most of the adult females did the same, with the exception of NU, who lip-smacked at the victim and went inside the gap, but I could not see whether she interacted there with the victim or not. She did groom and embrace another juvenile in the cavity where the victim was, while this was curled between them and the trunk. AU went into the cavity and bent over the victim, but it was not clear what she did. All the other females either looked briefly from the top of the buttresses or passed by without paying attention. It is worth noticing that in several occasions some individuals of R2 were again within less than 100 meters of the closest members of R1. Only a few sub-adults were seen, so

might had been better classified as a male incursion ² (Sicotte, Macintosh 2004) instead of an intergroup encounter.

At the end of the observation, while the victim is being attacked by a juvenile of roughly the same size as her, she manages to release herself and runs away, chased by a couple of juveniles. We could not find her again and there were no reports of an injured juvenile later that day in R2 nor the days after. We are uncertain whether she went back to her group or not. We were not able to see injuries during the observation.

² In my study, I consider as male incursions those situations in which a small group of 1-4 sub-adults, male juveniles and/or adult males of their leave their bi-sexual group and approach another group, staying in visual contact with them. They may interact with members of the other group by being affiliative and, more unfrequently, aggressively.



Figure III Snapshot of the attack by R1 to a R2 juvenile the 20th February 2016. AF= Adolescent female j; F= Adult Female; j=Juveniles; SA=Sub-Adult, M=Adult Male, V=Victim

Full description

It was the end of an encounter between R1 and R2. Me (LI) and JB were covering it when JM and MS let us know that a juvenile of R2 was trapped between the buttressed of a tree by R1. JB and I went there and I started recording the event at 11:14. There were about 20 monkeys within 3-4 meters of the trapped juvenile of R2, including 3 females (HS, NS, GU, VS, AU), 2 sub-adults (NK, XK), 2 unidentified adolescent females and many juveniles. It took time to find a proper place to observe the event, since the juvenile could hardly be seen between the buttresses and there were many individuals around, preventing me to get a bit closer.

At 11:17 I found a spot where I could observe a little bit better and focus on the individuals seated on the buttressed around the victim (Figure III, Picture 1). When I arrived to the spot these were: NK, NS, GU and at least 4 juveniles. NK seems to look inside the buttresses and to lunge at the victim in a couple of occasions. NS leaves and so has GU at some point; I can only see NK and a few juveniles within 1m of the space between the buttresses. NK leaves and an adolescent exits the space between the buttress, which is quickly occupied by a juvenile who seems to bent to bite the victim. It is quickly displaced by the adolescent previously mentioned, but what happens to the victim is obscured by another adolescent and XK who arrive and put themselves in front of the scene. NK comes back and another adolescent gets inside the space. Screams are heard in the video, but they come from behind the observer, not from the victim. XK leaves. An adolescent lip-smacks and presents at NK, who examines her genitals, but does not mount her and present her for grooming, which she does. After a while, IU approaches them and sits. KK approaches them displacing IU, who leaves. Then there is a coalition against one of the monkeys and the aggressions ends up being redirected towards me, so I stayed still until they calmed down.

I started to record again at 11:27 but I could find a spot to continue the observation until 11:30. A conversation with the observers following R2 revealed that the group was relatively close, enough as to be consider an encounter. Around the buttresses where the victim is, is possible to see NK being groomed, but no more than this. I stopped recording and went to check where R2 was. At this point JB had been less than 15 days in Tangkoko and was not ready yet to collect data, so she stayed watching whether the trapped R2 juvenile escaped or not while I checked the encounter. I did not see R2 close by, but I did see most of the group resting and grooming spread out around the tree where the juvenile was, for several tens of meters. At 11:37 I saw several sub-adults of R2 being monitored by NK, SK and XK. The rest of the group did not payed attention. It might have been an incursion of the sub-adults of R2, without the rest of the group. Since the trapped juveniles was a rare and relevant event, I continued recording the behaviors towards and around the victim.

I see KU and DU approaching the area where the victim is but then I go again to check for R2, which is still 20-30 meters from the closest member of R1, who is SK. Most of R1, however, is several tens of meters further away, mostly around the tree where the juvenile of R2 is being held, grooming and resting. KK goes within the buttresses, but I cannot see what happens there. There are several juveniles around the buttresses and some vocalize, but the visibility is not good.

I find a better spot and for a while I only see KK's back while he sits on the tree buttress looking down at the R2 juvenile. By zooming I see that someone else is with the juvenile in the cavity. I collect some data on the individuals around and when I point again the camera towards the buttresses, KK is gone and LK is inside the cavity and manipulating the victim, who does not resist nor looks alive. LK goes out of the cavity, but there is still someone else besides the victim inside, who seems to be manipulating the victim, but is difficult to tell.

After a while, NU approaches through a third buttress, look down towards where the juvenile of R2 is and lip-smacks. Then she leaves and QS passes by the buttresses. AK also has a quick look and leaves. Then I go again to check what the rest of R2 is doing. At 11:51, after looking around, I think the encounter is over and go back to where the trapped R2 juvenile is.

IB goes inside the cavity, but I cannot see whether she does anything to the R2 juvenile. I get into a better spot and I see another adolescent female biting the R2 juvenile. Around there is a juvenile and AU. Then the adolescent grooms the victim slightly. LK approaches and after looking from a buttress goes inside the cavity displacing the adolescent, who goes out and so does the juvenile. LK seems to bend towards the R2 juvenile, but only his back is visible. The adolescent that was attacking leaves the proximity. IB comes and LK seems to be grooming the victim. IB leaves. And a juvenile supplants her and presents to AU who grooms it.

A juvenile goes inside the gap while QS, who just approached, watches. Then I did a group scan before keeping recording the events around the R2 juvenile. BM has come within proximity but leaves shortly after. For a moment I see a juvenile in the cavity lip-smacking to NU, who goes inside and embraces it, and grooms it. Then an infant goes into the gap as well. Then, when NU stops grooming and presents I realize that the juvenile she was grooming was not the victim, who is curled and playing dead between the trunk and the juvenile she was grooming to. When NU leaves, the juvenile grooms the victim, who plays dead. Then the juvenile grooms himself and the scene is obscured by OU, who stands on the buttresses. Afterwards she goes into the cavity, the juvenile that was already there keeps grooming the victim and a male juvenile mounts OU and gets inside the gap before mounting her again. Then both leave the cavity and OU grooms the juvenile on the buttress before the cavity.

IB comes and looks inside the cavity. Another adolescent goes inside the gap, but I cannot see what happens there. A juvenile and the adolescent go out of the cavity and a big juvenile then goes inside and bites the victim. It is seen how he (it is a male juvenile) bites the R2 on the upper part of the mouth and rises it by it until its body is straight, before releasing it (Figure III, Picture 2). Meanwhile, another juvenile in the cavity watches the attack. They both go out shortly after.

After a while, an adolescent and IB go into the cavity. One seems to be biting the R2 juvenile, about the other is not that evident, but she bends over it as well. Then NU pulls IB's hair and IB leaves the gap. The other adolescent stays, but soon OU moves making the sighting more challenging. A juvenile descends then into the cavity, but I cannot see what happens inside.

When the juvenile leaves I manage to get a view of the victim, who seems dead, lying down on one side in the cavity. Then, it turns himself upside down and curls. Then an adolescent approaches it and touches it, even grooming slightly...before putting her foot on the victim's face. Then is not very clear whether she bites around the mouth or only sniffs the area, but she manipulates the head of the R2 juvenile with her hands. Shortly after a juvenile goes inside the cavity producing play grunts and they embrace. Another juvenile also goes with them. The adolescent mock bites the juvenile and then presents it for grooming, which it does. The victim seems to be between them and the trunk, but it is not visible.

NK approaches and goes inside the cavity but quickly leaves and goes out of sight. He is replaced by XK, who seems to manipulate the victim, but is obscured by the juvenile and adolescent grooming. Then XK goes out and sits on the buttress in front. After a while, PS appears and presents to XK, who ignores her. Then OS does the same and is ignored as well and leaves. An adolescent looks towards the cavity from one of the buttresses. Seems that someone is biting the victim inside, but it is not possible to see clearly with XK in front. Juveniles stand on the buttresses looking towards the victim. XK goes inside and seems to bite the victim. KU watches as well and then one of the male juveniles aggresses GU, who moves away and screams at him asking for support. Nobody comes and she leaves. The male juvenile does the same to another juvenile, that also screams and ask for support but is ignored as well. And again, the male juvenile tries to hit another juvenile and threats it. Meanwhile, he is covering what happens within the buttresses.

CU passes by and stops a moment to look inside the cavity before leaving. When the male juvenile finally moves away, it is possible to see XK grooming the juvenile of R2, while the adolescent female who was also inside watches him doing so. He stops and gets out, displacing another adolescent who was sitting on the buttresses. He obscures the sight into the cavity. The adolescent leaves too. Shortly after is possible to see a male juvenile biting and rolling the victim. The R2 juvenile does not struggle and plays dead. The juvenile keeps manipulating the victim's body, turning it upwards and pulling its legs up, biting and dragging it. XK goes in and then is possible to see the victim lip-smacking at him, but XK bends and apparently bites.

Then he goes out and sits on the buttresses in front. The juvenile then starts biting the victim again, pulling its head upwards.

QS comes and presents to XK, who ignores her and present her for grooming. She ignores him as well and leaves. The juvenile that was attacking the victim goes out of the cavity. Then we see that apparently there was another juvenile inside, which is now pulling the victim's hair, moving its whole body at its wish. Again, the victim does not resist at all and stays immobile facing down. Another individual gets inside the cavity, but cannot be seen with XK in front. It was a male juvenile, who quickly jumps out of the cavity and sits on one of the buttresses. A couple of juveniles look inside the cavity standing and XK masturbates. Then he goes into the cavity and seem to do something to the victim, but is not visible. An adolescent female approaches and sits on one of the buttresses.

AU and TM approach and look inside the cavity. TM loses interest almost immediately while AU still peers inside. QS approaches XK and presents. QS leaves and XK follows, AU sits where he was, facing the cavity. The juvenile inside manipulates the victim's body, pushing and biting it (Figure III, Picture 3). A couple of juveniles and an adolescent stay around the buttresses. Two juveniles mount the adolescent successively.

I notice that several individuals seem to be monitoring. I stop following the event of the trapped juveniles to check whether anything else is happening and soon go back after not finding anything unusual. When I continue the observation, EJ is sitting on the buttresses and looks towards the cavity, where some individuals seem to be biting the victim. A couple of juveniles and an adolescent watch the aggression from the buttresses and so does LK. DS passes by over the buttresses without paying attention to the attack. EJ leaves and a juvenile goes into the cavity, in which there is already a couple more. NU sits on the buttress facing the cavity. OU and a couple of adolescents are also on the buttresses over where the victim is. Nothing inside the cavity is visible. OU leaves and so does one of the adolescents. AU goes into the cavity and bends over the victim, but does not seem to aggress it. Then she goes out and sits close. BM arrives and looks into the cavity. There are several juveniles inside around the victim, who cannot be seen. BM sits and grooms someone on the buttress. A male juvenile goes out of the cavity. Super-nose climbs the buttress and looks inside the cavity; then leaves.

SN stands over the buttresses and peers inside the cavity as well, then approaches BM, displaces him and supplants him. OS approaches and presents to SN who examines her and starts grooming her. A juvenile seems to be in contact with the victim inside the cavity. Then it leaves. The victim then seems to

be alone in the cavity. It sits down and lip-smacks nervously (Figure III, Picture 4). SN looks towards it. The juvenile seems to be a female (1:14:00 in the video). A juvenile goes inside the cavity and bites her on the throat (Figure III, Picture 5). While the juvenile was trying to pull from the victim's back, it finally jumps out of the cavity and runs away from R1 (Figure III, Picture 6). A couple of juveniles chasing her. We search but we couldn't find the juvenile again. No injured juveniles were reported in R2 and we are uncertain whether it came back to its group.



Figure IV Time-diagrams of the attack on juvenile female from non-habituated group by R1 (20th February 2016)

29TH APRIL 2016 CASE: UNKNOWN FEMALE AND R1*Summary***Observer/s:** LI, JB (MT)**Victim:** Adult female from unhabituated group**Aggressor group:** R1

While R1 was having an encounter with a non-habituated group, a female of the other group ended up surrounded by R1 and stay the once the unknown group had retreated. JB started the recording of events at 10:27.

At the beginning of the observation, she was curled up between the buttresses of a tree with 2 sub-adults, KK and MB, as well as some juveniles looking at her. Soon, however, adolescents and females joined the observation. Most females that passed by did not pay much attention to the victim, and at most, the examined her. The only exceptions were VS and NS, who approached briefly, bit her and leave again. IU, on her part, groomed the victim slightly. KK attacked the female as well, but just in a couple of occasions at the beginning. The bulk of the observed attacks came mostly from two unidentified adolescent females who bit the female repeatedly, to the extent of dragging her body with their mouths. Several juveniles participated too, examining, biting and even leaning on the female. The victim did not struggle at any point and played dead most of the time. The exception was a point in which there was a strong noise and she made an attempt of standing. However, she stopped herself in the middle of the action, after attracting the attention of IU and a juvenile, who approached her as soon as they saw her moving.

Interestingly, around the middle of the observation, LK approached the female and sit nearby, after which the attacks toward her almost completely stopped and the macaques nearby were sat around without paying attention to her. During this period, LK mostly self-groomed while keeping body contact with the female by putting his leg over her head. Later on, MM would approach and smelled the female and joined that sort of “guarding” with LK for a while, before running towards a conflict. Afterwards, NK displaced LK and occupied his position, again not aggressing the female. Most of the monkeys around did not try to interact with the victim at this point and sometimes, if someone tried, it was threatened by NK and retreated. NK lip-smacked at the victim in a couple of occasions.

Finally, the female stood up and started walking away slowly before fleeing at full speed. She was chased by NK, LK and a juvenile. We (JB,LI,MT) tried to find her again, but we unable. We were not able to see injuries during the observation.



Figure V Snapshots of the attack by R1 to the unknown female the 29th April 2016, in chronological order from top to bottom and left to right. AF= Adolescent female ; F= Adult Female; j=Juveniles; SA=Sub-Adult, V=Victim

Full description

While R1 was having an encounter with a non-habituated group, a female of the other group ended up surrounded by R1 and stay the once the unknown group had retreated. JB started the recording of events at 10:27 (03:06 in her video).

At the start, the female lies motionless between the buttresses of a tree, in front of which are Mowgli and Lucifer. Lucifer threats someone outside the video frame and leaves, presumably to chase it. Kevin appears, approaches the female and manipulates her body, turning it around and examining it. The female keeps being still. Iris passes by and stops to have a look at the female. Kevin bites the female on the flank. Mowgli and Iris leave and while Xiro approaches, the female moves the head to look around. Her breath seems quick. Xiro smells her genitals and then touches her (Figure V, Picture 1). She curls up and Kunti approaches her. Kunti touches her and Xiro pulls from the fur of the victim's back several times. A juvenile, Juni and an adolescent approach the female (Figure V, Picture 2) and Xiro leaves. Then another juvenile comes close. It is possible that they are all touching her and maybe some even biting, but is not possible to know for certain since they cover the view. Then the last juvenile to join the mob, a male, drags her toward him, makes her sit and bites her throat. An adolescent (we don't know her name, but is possible to ID during the video and will be referred here as af1) pulls her away from the juvenile and bites her. Kunti has left and Helicopter comes to watch. The adolescent seems to bite a couple of times. Ani passes by, looks and continues her way. The adolescent leaves. Xiro approaches and touches the female and a second adolescent (same situation as with the previous adolescent and called during this description as af2) does the same. The af1 comes and grooms the female for a couple of seconds before manipulating her body while the af2 bites the victim's face. The af1 and 2 juveniles bite the female too. Caca appears and watches. The af2 bites again fiercely on the back. The female does not struggle at any point but sometimes seems to try to curl up more. Helicopter, who appears again, watches. Caca, af2 and Helicopter leave. The female lies motionless facing the ground. Juni and a male juvenile approach. Juni examines the victim while the juvenile bites her. The af2 displaces the biting juvenile and bites the female, dragging and shaking her. Xiro approaches and touches the female. Xiro leaves and a juvenile grooms the female. Then af2 bites her again.

Nihil approaches, smells the female and touches her, almost grooming. She leaves when the af2 comes again and bites the female. Three juveniles examine the female and touch her. Ani approaches, grabs the crest of the female and pulls a bit from it, apparently to see her face. The af2 tries to affiliate with Ani and Ani leaves. The 3 juveniles keep examining the female, one grooming her. Vodka approaches and

smells but is displaced by Juni, who also smells the female. The af2 comes backs, takes a tumble over the female and embraces Juni (Figure V, Picture 3). Meanwhile, the juveniles keep examining the victim's body. One of them leans on her before grooming her briefly. Ani and Paulina approach. Paulina examines the female while Ani embraces a juvenile. Leoni approaches the female, examines her and smells her and then Paulina leaves. Leoni follows. Nihil approaches and smells and so does Nuria, who bites her slightly before leaving followed by Nihil. Martabak appears and leaves. The af1 takes one of the legs of the female and drags her. Then she pauses before dragging her by an arm, which the af2 bites. Iris approaches and turns the female around pulling her arms. The af2 bites the female while some juveniles approach and examine her. Nihil approaches, takes the victim's arm and smells her flank. Two juveniles groom the female briefly. Then a juvenile bites the female's head and so does the af2, on the face. A juvenile bites the female back. After a pause, the af2 bites the female's back again. Leoni approaches and smells while a juvenile bites the female. Leoni touches the female, Nihil smells her and leaves. 8 juveniles and Leoni surround the female. A juvenile grooms her back. Leoni leaves. Iris approaches and drags the female after smelling her. A juvenile bites the female's back. Iris retreats and Kunti approaches. Uhnir comes near the victim and smells her. The af2 approaches and bites the female several times. Then the af1 approaches and does the same. The af2 bites the victim's leg and drags her. The af2 leaves and a juvenile grooms the female. The af2 comes back and bites, then leaves, comes back and bites her again before dragging her. Then pauses, bites her once more and leaves. Five juveniles and the af1 are still around her. Intan approaches and smells. A juvenile touches her and lies by her side. Another bites her playfully. The af2 approaches and bites the victim's mouth. Then bites her back and drags her. The af2 bites the female again and a juvenile does the same (Figure V, Picture 4). The af2 bites the female's face again and drags her. Then Vodka bites the upper part of the female's head and drags her. A juvenile bites the female. After a pause, the juvenile and the af2 bite the victim again. Then, the af2 displaces the juvenile to bite where it was biting and takes a tumble over the female. Two juveniles groom the female. One of them leaves and the other continues. Kunti approaches and smells the female. A long time passes with Vodka, Kunti, af1, af2 and several juveniles around the female without attacking her. Then af2 and a juvenile bite her again.

Lucifer approaches, sits and briefly grooms the female, Kunti leaves. Lucifer stays by the victim grooming himself. The af2 approaches but retreats when Lucifer looks at her. Later, a juvenile tries to approach but moves away when threatened by Lucifer. Later he lunges to a juvenile nearby, who goes further. When he does that, the female reacts and straitens a bit and looks around. A juvenile and Intan approach her and examine her. Then the af2 bites her on the face and drags her. A juvenile grooms the female and then bites her. Intan smells the victim's anal area. Later on, a juvenile put itself over her, then tries to turn her around and bites her. Then a juvenile grooms her slightly. Only Lucifer, Intan and 2 juveniles are within 1 meter of the victim. Lucifer approaches the female displacing the juveniles that were close to her and sits next to her, with one of his legs over the female's head. Both juveniles and Intan leave and

Lucifer grooms himself. Martabak approaches and smells the female before sitting close to her. Lucifer pets her back.

Af1 approaches and examines the female. She sits for some seconds and then leaves the proximity of the female. For a long time only Lucifer, self-grooming, and Martabak, monitoring the surrounding area, stay in close proximity with the female, who lies down playing dead. Then Martabak runs towards a conflict out of sight. Then af2 approaches and looks at the female before sitting within a meter. A bit later a juvenile joins the af2. Lucifer has his leg over the female's head still. Niko approaches and smells the female, displacing Lucifer, who leaves the close proximity of the female and sits within 2 meters of her and NK. The af2 smells the female and then bites her quickly in the leg, retreats and a bit later gets closer again and smells the genital-anal area. Niko smells and touches the female. After a while the af2 leaves the proximity of the female. The juvenile in proximity is a male.

Another juvenile approaches, presents to Niko, Niko presents for grooming and the juvenile grooms him. The juvenile male smells the hindquarters of the victim and so does another juvenile male who approaches. The af2 does the same. Then Niko threatens them and the juveniles retreat. The af2 touches and grooms the female, not very perturbed by Niko's threat. Then she leaves the close proximity of the victim.

A couple of minutes later, Caca approaches and presents to Niko, standing over the female (Figure V, Picture 5). Niko examines Caca but rejects. Then Caca grooms the female briefly before leaving.

Niko lip-smacks to the female. A juvenile approaches and Niko lies down and approaches his face to the female. The juvenile who was grooming Niko stops and leaves. Niko lip-smacks and the other juvenile leaves.

Niko seems to do either lip-smacking or sexual jaw movement to the female. He lip-smacks a bit later. Then the female stands and slowly starts to move away with silent bared teeth, before fleeing (Figure V, Picture 6). Niko, Lucifer and a juvenile run behind her. We couldn't find her again.



18TH JULY 2016 CASES:

At 13:09, we (LI & JB) perceived that many individuals of our focal group ran towards the beach. I followed them and see that PB1 was there, fleeing towards the East. Most of PB1 managed to escape. However, several individuals were kept by small groups of R1 macaques. JB and I followed as many cases of such harassments as possible (5), as reported below.

Emping and her infant

Summary

Observer/s: LI & JB**Victim:** Adult female (Emping) and her infant, from PB1

This one was the first mob that I (LI) approached. I found MM, TS, OU, PS,YS,VS,LS and 2 juveniles around a pool filled with water on the rocks by the beach. Inside the pool was Emping with her infant.

For a bit less than 10 minutes, several juveniles, LS and OU grab Emping and pull from her arms and bite her. Some juveniles try to touch the infant as well. Emping does not resist and does not move except to cover the infant once that is exposed. She defecates several times. Her infant swims in the puddle but remains close to her mother and grabs her fur when possible. Eventually, with the pool surrounded by several R1 monkeys, Emping jumps out from the pool and flees carrying her infant.

However, she is chased by CB and juveniles, who finally catch her and presumably aggress her, but cannot be confirmed since all formed a huddle around her. Soon she jumps to the water and swims to a nearby rock while her infant stays behind. She is soon attacked by an adolescent and juveniles and ends up swimming to another rock. Meanwhile her infant is bitten and licked by LK. The infant protests every time anyone touches her and moves towards the forest whenever is left free. She also lip-smacks when another monkey looks at her. Nuria suddenly approaches and bites the infant violently, but a wave breaks and everyone around the infant leave, realizing her.

While she keeps moving slowly towards the forest, her mother jumps again into the sea when AS, KK and CB chase her. She swims away. I continued following another coalitionary attack on a juvenile (see below).

Emping reached the place where JB was recording the aggression on GA (see below). There the aggressors were a juvenile, MB and LK. Interestingly, when is attacked by LK at a point in which the other 2 R1 members are out of sight, she resists, releases herself by struggling, and screams while lunging at LK, before retreating and going behind GA. LK grabbed her again and she resisted, screaming and even hitting LK. While they are fighting, MB grabs Emping's crests and pulls, making her to fall back. This is a striking difference if compared with her aptitude at the pool.

Soon after, the 3 R1 macaques leave and Emping swims away. Once she on the nearby rocky beach, she is chased by juveniles and runs towards PB1. She reaches them and joined them successfully. No injuries were reported for her.

Her infant managed to get to the forest and after about an hour, she was "adopted" by AU, meaning that AU carried her and protected her if someone tried to approach her. However, the infant died one day later. AU carried her one more day after that.

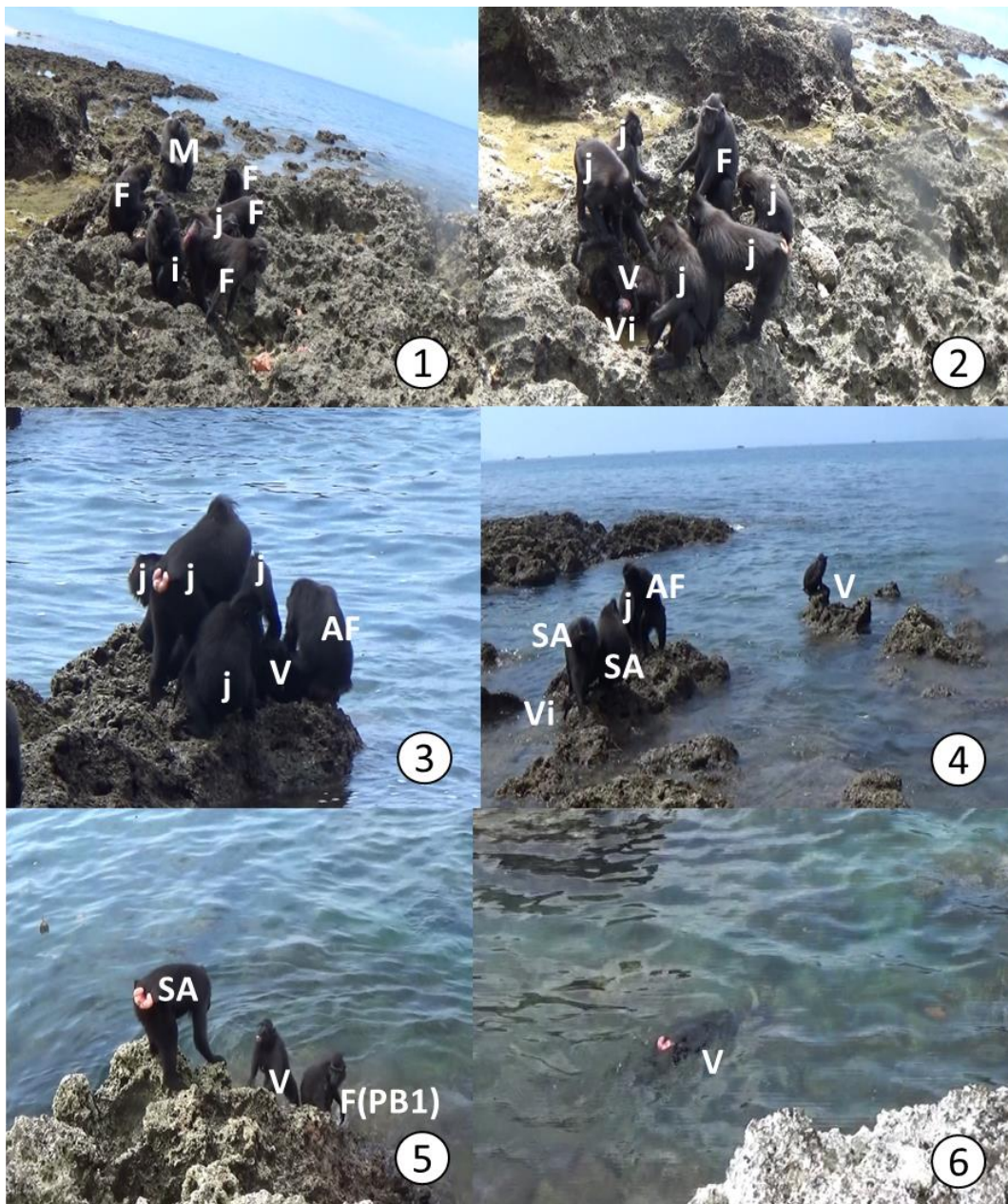


Figure VII Snapshots of the attack by R1 to Emping the 18th July. AF= Adolescent female); F= Adult Female; j=Juveniles; SA=Sub-Adult ; V=Victim ; Vi= Victim's infant ; M=Male

Full description

This one was the first mob that I approached. I found Martabak, Tuti, Ola, Paulina, Yane, Vodka, Leoni and 2 juveniles around a pool on the rocks by the beach (Figure VII, Picture 1). Inside the pool was Emping with her infant. Shortly after I arrived, Yane, Vodka and others run towards another individual of PB1 who could have been Gluten (see below for her the attack against her). Leoni is the only one staying by the pool, and bends to reach Emping and bite her. Ola comes back with her infant and a juvenile and does the same. Kunti, Martabak and a juvenile approach too. The observation is then briefly interrupted when another mob is detected and I call JB to cover it. For a while, Emping and the infant are left alone, with her apparently paralyzed and crouched on the pool. Only Ola and the baby are at the edge of the pool and some juveniles are visible as well, observing what is happening on the other side of the beach. Emping's infant climbs to her mother's back and then Leoni and 2 juveniles approach, after which Ola leaves with her infant. A juvenile and Leoni reach out to Emping and the baby and touch them. The other juveniles approach and watch the infant. One of them bents and lip-smacks at it. Emping defecates several times. Other than that, she does not struggle when the macaques of R1 grab her. Leoni reaches her and touches her slightly. Later she grabs Emping's hand and pulls, making her to sit down on the pull. Emping looks around. A juvenile grabs the fur of her back and pulls towards itself. Then it pulls her arm and bites it. Emping does not resist. Another juvenile touches Emping's head. About 1-2m from the pool, Vodka embraces Ola and then Leoni approaches them and embraces Vodka. Meanwhile, a juvenile bites Emping. When the embrace is over, Vodka approaches Emping vocalizing and pulls the fur from Emping's back and makes her to look at her. Leoni leaves and a juvenile pulls from Emping's arm several times. Emping doesn't resist and breaths quickly. A juvenile pulls her arm again while another pulls the fur of her back until they turn her around, leaving the infant exposed (Figure VII, Picture 2). Then one of the juvenile rubs the infant's face and pulls Emping's and her infant's arms. When they stop pulling, Emping curls, hiding the baby under her as she was doing before. Both of these juveniles were females. One of them pull from her again. Then Leoni pulls too and a juvenile seems to bite Emping. Around 13:17 the observation stops for a moment to watch another coalitionary aggression happening far away, where Mowgli and an adolescent seem to be aggressing a juvenile. I continue observing the case of Emping and her infant. Two juveniles and Leoni grab Emping's fur and pull from her to different sites vocalizing. When they stop, Emping jumps out of the pool and runs away towards the sea, chased by several juveniles and carrying her infant. Caca catches her and bites her. Emping shows no resistance. Several juveniles approach and seem to touch Emping and her infant. One of the older juveniles seems to be biting one of them, but is obscured by the presence of the others (Figure VII, Picture 3). Another adolescent joins, Caca bites Emping or her baby and some juveniles seem to be doing the same. The infant screams. Then Emping jumps to the water and swims to the next

rock, leaving her screaming infant behind. While several individuals surround Emping, Lucifer takes the infant and pushes it onto the rocks while the infant protests. Emping is left alone (Figure VII, Picture 4). Lucifer bites the infant's back, which makes her complain complains. An adolescent seems to lip-smack towards Emping. Then an old juvenile jumps towards Emping, grabs her crest and pulls her into the water. Meanwhile, Lucifer licks the infant. Then, once Emping gets out of the water, an adolescent jumps to the rock Emping is on, grabs her crest and pulls down. Emping does not resist. Lucifer keeps licking the infant's back while grabbing it with both hands. The infant lip-smacks at Mowgli who seems to lip-smack back. Lucifer bites again the infants back with the side of his mouth. A juvenile approaches the infant and seems to bite as well. The juvenile screams. Then both release the infant, who jumps to another rock towards the forest, but Lucifer follows it and presses it towards the ground. Then Lucifer bites the infant's back superficially. The infant complains. Meanwhile, Vodka and a juvenile are biting Emping, who jumps to the water and goes to another rock.

Lucifer bites the infant superficially and then holds it back by grabbing its leg. Vodka approaches the infant and lips-smacks at it. Then Lucifer bites the infant while it complains and Vodka vocalizes. Lucifer pulls the infant off the ground, Vodka touches it and then Nuria approaches and bites the infant on the neck violently. A wave breaks and makes all the monkeys on sight to run away in towards the forest. The infant lags behind and is caught by Lucifer, who bites it again. Then Lucifer leaves and the infant seems dead, but soon it stands up and walks towards the forest. Meanwhile, her mother is coming out of the water and alone, looking towards the forest. The infant keeps moving slowly towards the forest and lost-calling, sitting and lip-smacking if a monkey of R1 looks at her. Then Caca, Kevin and Ani run towards Emping, who jumps into the sea before they can catch her and swims away. Shortly after I detected the attack on the juvenile (see below) and followed it.

Eventually, Emping arrives where JB is recording the attack on Gluten (see below) around 13:25. Emping swims up to the rocks where Gluten is and sits close to her. The only members of R1 near them are Lucifer, Mowgli and a juvenile. Soon after reaching the rocks, Lucifer and the juvenile threat Emping and she does silent teeth-bared. The juvenile approaches her and seems to aggress her. He repeats the operation later on, hitting Emping's head with his hand flat. The juvenile leaves and so does Mowgli. Then Lucifer approaches Emping. He grabs her by the crest and pulls down to bite her neck. She screams and struggles and manages to release herself (Figure VII, Picture 5) and go behind Emping. The juvenile and Mowgli appear again and Lucifer grabs Emping again and bites her several times while she screams and struggles. Then Mowgli approaches and hits her. Lucifer releases her and Mowgli grabs her crest and makes her fall while she screams. After that, both sub-adults retreat and so does the juvenile after lip-smacking at Emping. The sub-adults leave and shortly after, Emping jumps into the water and swims and dives away (Figure VII, Picture 6) Once she on the nearby rocky beach, she is chased by juveniles and runs towards PB1. She reaches them and joined them successfully. No injuries were reported for her.

Her infant was bitten several times by Lucifer, who also licked her (Figure VIII, Picture 1i). Nuria bit her too (Figure VIII, Picture 2i), until a wave made the surrounding monkeys escape, leaving the infant lying on the ground apparently dead (Figure VIII, Picture 3i). Eventually, she stood up and walked towards the forest (Figure VIII, Picture 4i). She was “adopted” by AU, meaning that she carried her and protected her if someone tried to approach her. However, the infant died one day later. AU carried her one more day after that. The body was recovered but had been dragged after the death of the infant, so it was not possible for us to assess the *pre-mortem* wounds. We followed the infant after the encounter and the next 2 days until the body was recovered. This material will hopefully be released in a not too far future.



Figure VIII Snapshots of the attack by R1 to Emping's infant the 18th July. F= Adult Female; j=Juveniles; SA=Sub-Adult ; V=Victim

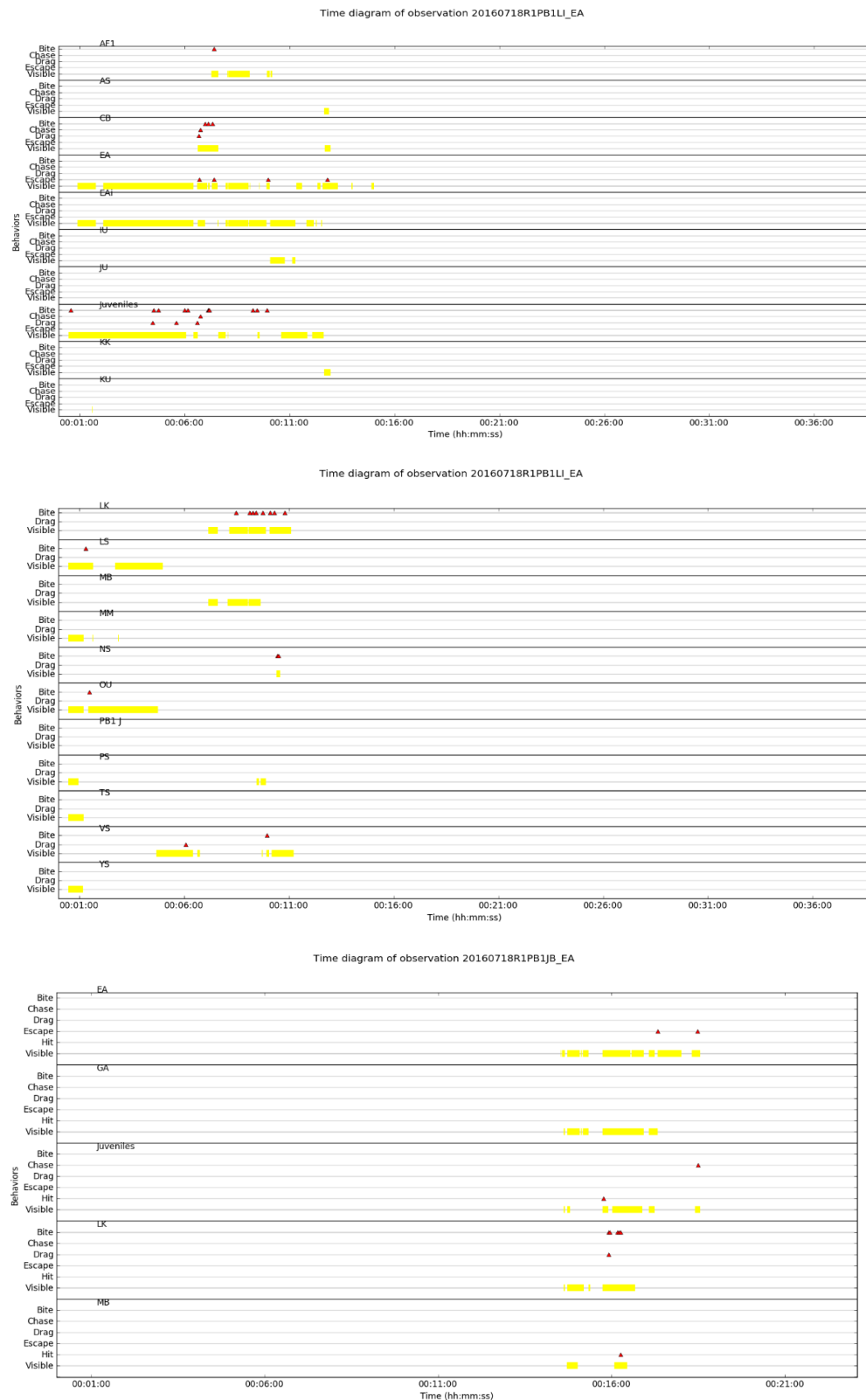


Figure IX Time-diagrams of the attack on Emping and her infant by R1 (18th July 2016)

Gluten

Summary

Observer/s: JB**Victim:** Adolescent female (Gluten) from PB1

JB arrived to a mob where AU, HS, CB, KK, OM and several juveniles are surrounding GA, who is not visible under them. It is possible that OM aggressed her, but he is only seen bending over her and leaving shortly after. She soon manages to escape, but is chased by KK and 2 juveniles. She is touched and aggressed by them. At some point, SK approaches her and s seems to only direct some facial expressions at her (not visible). She grimaces. When he attempts to get closer, she screams and avoid him, to which SK responds retreating and leaving. KK comes back and aggresses her several times, to what GA responds resisting and even hitting him. A juvenile aggresses her as well. MB appears and so does PS, who bites her.

Shortly after, Emping (see above) appears swimming. LK, a juvenile and MB are now the only R1 macaques near them. The juvenile grabbed GA and bit her. Later the three of them retreated, Emping swam away and GA flees towards PB1 and out of sight. She joined them successfully and no injuries were reported.

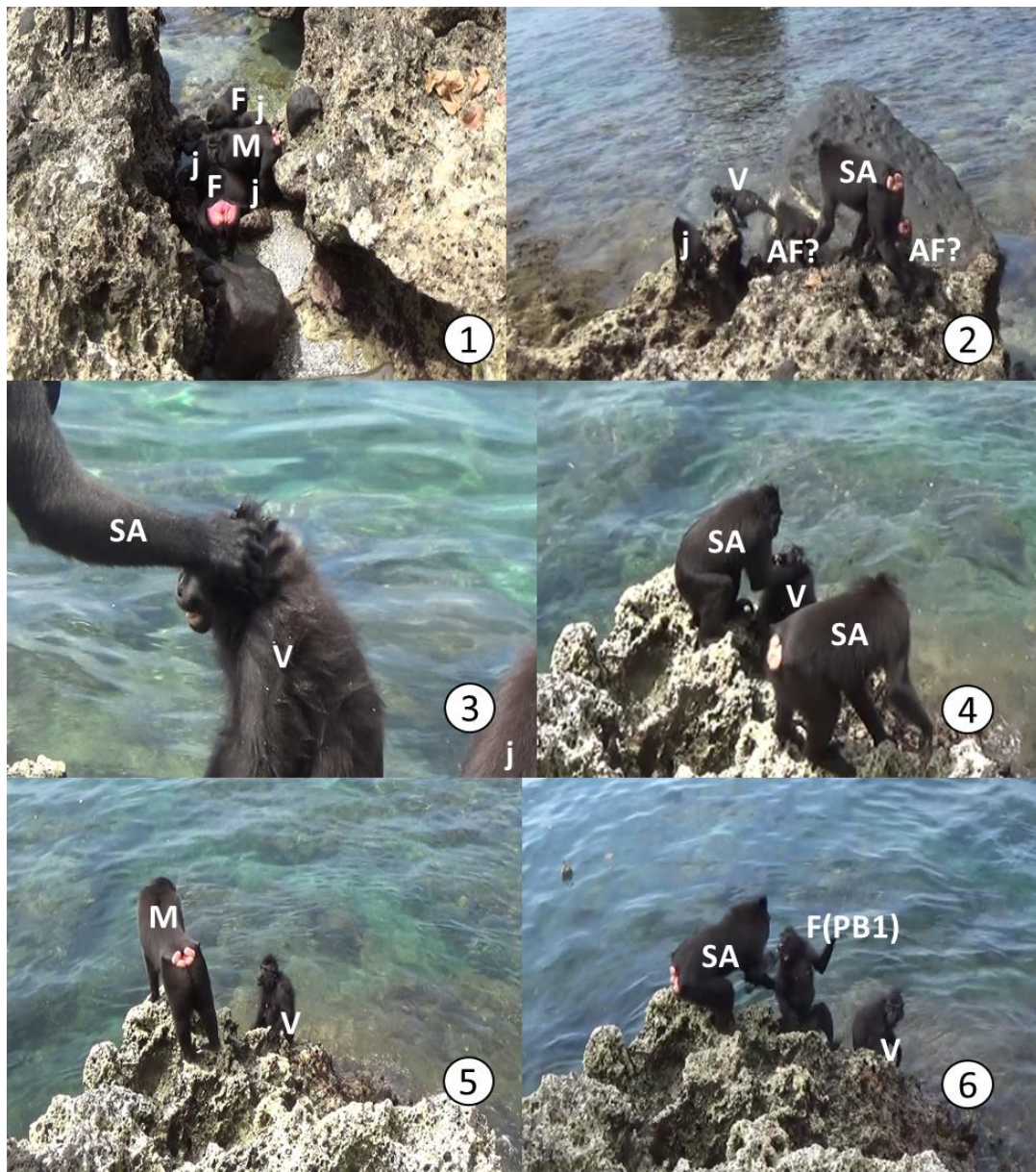


Figure X Snapshots of the attack by R1 to Gluten 18th July. AF=Adolescent Female F= Adult Female (EA , the female from the previous case) ; j=Juveniles; SA=Sub-Adult ; V=Victim ; M=Male

Full description

At 13:11, JB arrives to a mob where Adinda, Helena, Caca, Kevin, Probosis and several juveniles surrounded Gluten (Figure X, Picture 1). It seems that at least the 2 juveniles are attacking her, either pulling her hair or biting (they are on top of her and is not visible). Probosis is bent towards her and might be biting, but it is again obscure by the bodies of the others. Probosis leaves and the others diminish their

attack and Gluten escapes (Figure X, Picture 2), but is chased towards the sea and surrounded again, this time by Kevin and 2 juveniles. She half-open mouths and Kevin touches her head several times (Figure X, Picture 3). Then he goes a bit further and a juvenile approaches her and touches her. Kevin grabs Gluten and pushes her head down. She screams and struggles. Caca approaches and bites her. Then she leaves and Kevin approaches again, grabs her and forces her to look at him (Figure X, Picture 4), after which he retreats. He approaches again, touches her head and leaves.

Solo approaches and Gluten opens-mouths at him and avoids him. Solo stands close to her and seems to direct facial expressions at her (but is with his hindquarters towards the camera, it is not possible to see his face) (Figure X, Picture 5). He lunges at her and she screams and avoids. Then Solo leaves, Kevin approaches, stands, yawns and leaves. Shortly after he repeats the same. Then he comes back, grabs her and tries to bite while Gluten screams and struggles. There is no one else nearby. He leaves and approaches again, grabs her by the crest and pulls towards her back. Then he retreats again. A juvenile approaches her, examines her and when he tries to bite her, she screams, struggles and hits it. Then the juvenile retreats and Kevin pushes her head down violently. Then grabs her face and makes her look at him and then bites her while she screams and struggles.

After a moment covering the attack on Yams, the observation continues with Gluten, who screams as Mowgli approaches threatening her. She retreats. Paulina and Mowgli approach and Paulina grabs Gluten's face and bites her. The juvenile bites Gluten too. Then Paulina leaves. After a while the juvenile male goes close to Gluten, turns her around and bites her back softly before retreating. Lucifer approaches her and directs some facial expressions at her, but is not possible to see which ones.

At this point, Emping arrives swimming and sits close to Gluten. While Lucifer attacks Emping, Gluten retreats slightly and looks towards them (Figure X, Picture 6). A juvenile male approaches Gluten, grabs her and bites her while Gluten struggles. Mowgli and a juvenile retreat, leaving Emping and Gluten alone with a male juvenile, who retreats shortly after. Emping escapes swimming and then Gluten flees towards PB1 and out of sight. She joined them successfully and no injuries were reported.

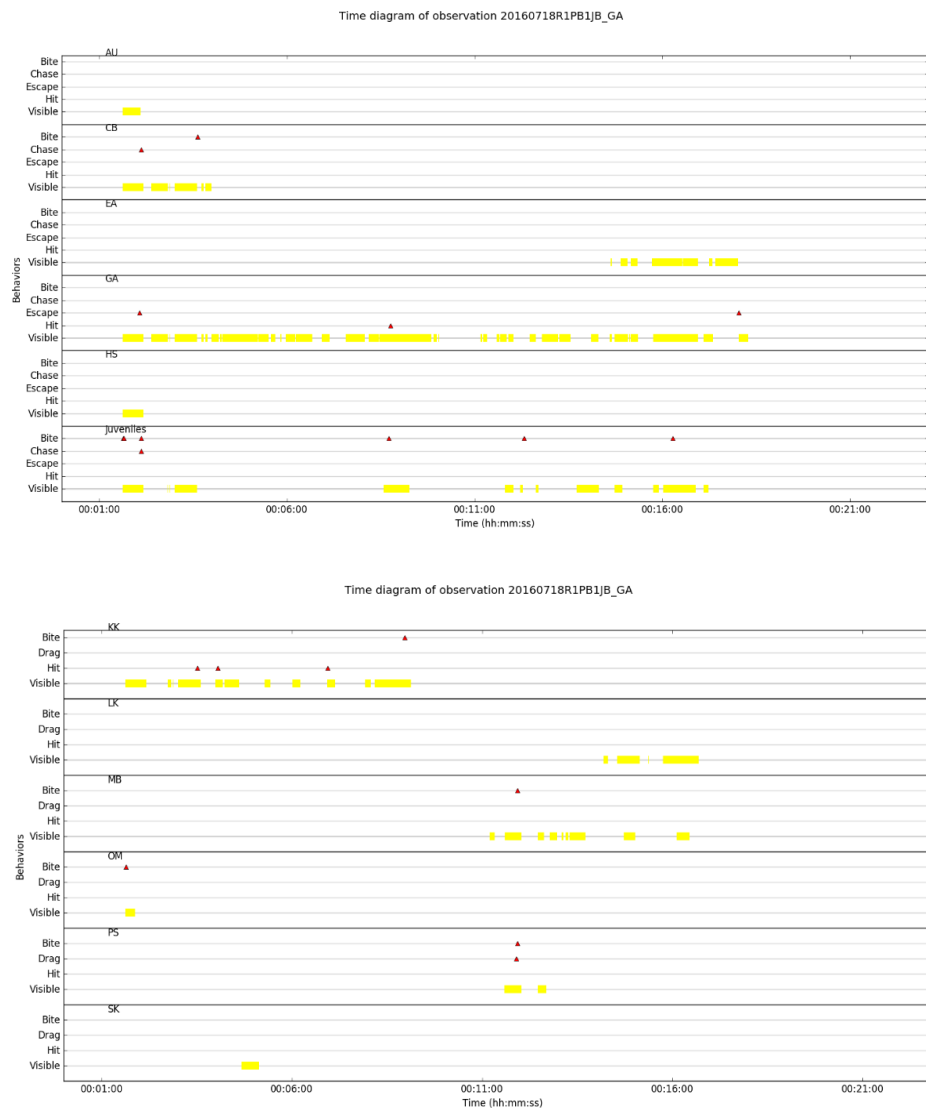


Figure XI Time-diagrams of the attack on Gluten by R1 (18th July 2016)

Female juvenile from PB1

Summary

Observer: LI**Victim:** Juvenile female from PB1

After Emping had been separated from her baby, with the infant going towards the forest, I encountered another mob attacking a juvenile from PB1 (13:23). The juvenile screamed while a juvenile and Nuria bit it and two females (Intan and Juni) were bystanders, together with some more juveniles. The juvenile struggled and managed to free herself and run, but was soon trapped again. She screamed and did silent bared-teeth to the monkeys of R1 who tried to approach her. CB and KK were the most aggressive towards her, by following her from rock to rock in which she tried to swim away from them, biting and hitting her and pushing her into the water. Ani bit her once as well. The juvenile from PB1 ended up swimming up to the rocks in which Emping and GA had been before and was attacked there by several juveniles, who hit her and pushed her into the water. In the end, she managed to rejoin PB1. 4 juveniles in PB1 were reported to have injuries that day.



Figure XII Snapshots of the attack by R1 to a juvenile female from PB1 the 18th July. AF=Adolescent Female F= Adult Female; j=Juveniles; SA=Sub-Adult ; V=Victim ;i=Infant

Full description

After Emping had been separated from her baby, with the infant going towards the forest, I encountered another mob attacking a juvenile from PB1 (13:23). The juvenile screamed while a juvenile and Nuria bit it and two females (Intan and Juni) were bystanders, together with some more juveniles (Figure XII, Picture 1). The juvenile was most likely a female, since the groin is visible several times in the video and no sexual organs are seen (Males have pink genitals, easy to spot since they are born). Two juveniles and CB grab the juvenile from PB1 while she tries to escape. The juvenile from PB1 screams and struggles. She manages to release herself and runs away a few meters, but she is chased by several juveniles and Caca and then pushed into the water (Figure XII, Picture 2). There, it has a break from the attacks, since R1 seems to be unwilling to venture in the water. They stand lip-smacking at her and approach her, trying to not touch the water. At some point, the juvenile from PB1 sits on a rock and a juvenile from R1 comes and grabs one of her arms, just before Ani comes and bits her on the arm, while the juvenile from PB1 screamed (Figure XII, Picture 3). An adolescent comes then and while trying to grab the juvenile from PB1, she allows her to escape swimming into the water until she reaches another rock on the surface. Then she moves to another where a juvenile embraces her. The juvenile from PB1 tries to avoid it though. Then the juvenile of PB1 is left alone for some moments, before Caca jumps to the rock she is on, followed by Kevin. As a response, the juvenile from PB1 moves away of the rock, goes into the water and screams. Kevin jumps up to where the juvenile is, pushing her towards a deeper place while the victim screams and he hits her, making her sink (Figure XII, Picture 4). The juvenile tries to swim toward another rock but Kevin hits her again, pushing her into the water. The juvenile swims away from Caca and Kevin. Caca approaches it, but then the observation is interrupted to look for Empings baby and by the detection of another mob. When the observation on the juvenile from PB1 continues, she is on a rock surrounded by water and Caca and an old juvenile, possibly Qubes, jump onto the rock and bite her (Figure XII, Picture 5). The juvenile struggles and jumps to the water. Kevin leaves and the juvenile swims to the rock Caca is on. She sits close to her and lip-smacks. Then Caca leaves and the juvenile stays on the rock. The observation is then interrupted to follow the one against Yams, and only checked at intervals. During one of those, Lucifer and a juvenile direct facial expressions towards the juvenile from PB1, but is difficult to see which ones. The juvenile swims towards another rock and screams when several juveniles threat her at her arrival. A juvenile grabs the victim and hits her (Figure XII, Picture 6). The victim screams and lip-smacks. Another juvenile approaches and after lip-smacking at the victim, it grabs it and pulls from it while the victim screams. The observation is then interrupted again to check for Emping's infant. When I come back, I see blood on the rocks around the juvenile from PB1, which is now alone. A juvenile comes, grabs her and the juvenile from Pb1 ends up in the water again. It comes up and the juvenile of R1 leaves. The

observation was then interrupted to check others and shortly after all PB1 retreated. The juvenile was seen fleeing towards them. 4 juveniles in PB1 were reported to have injuries that day.

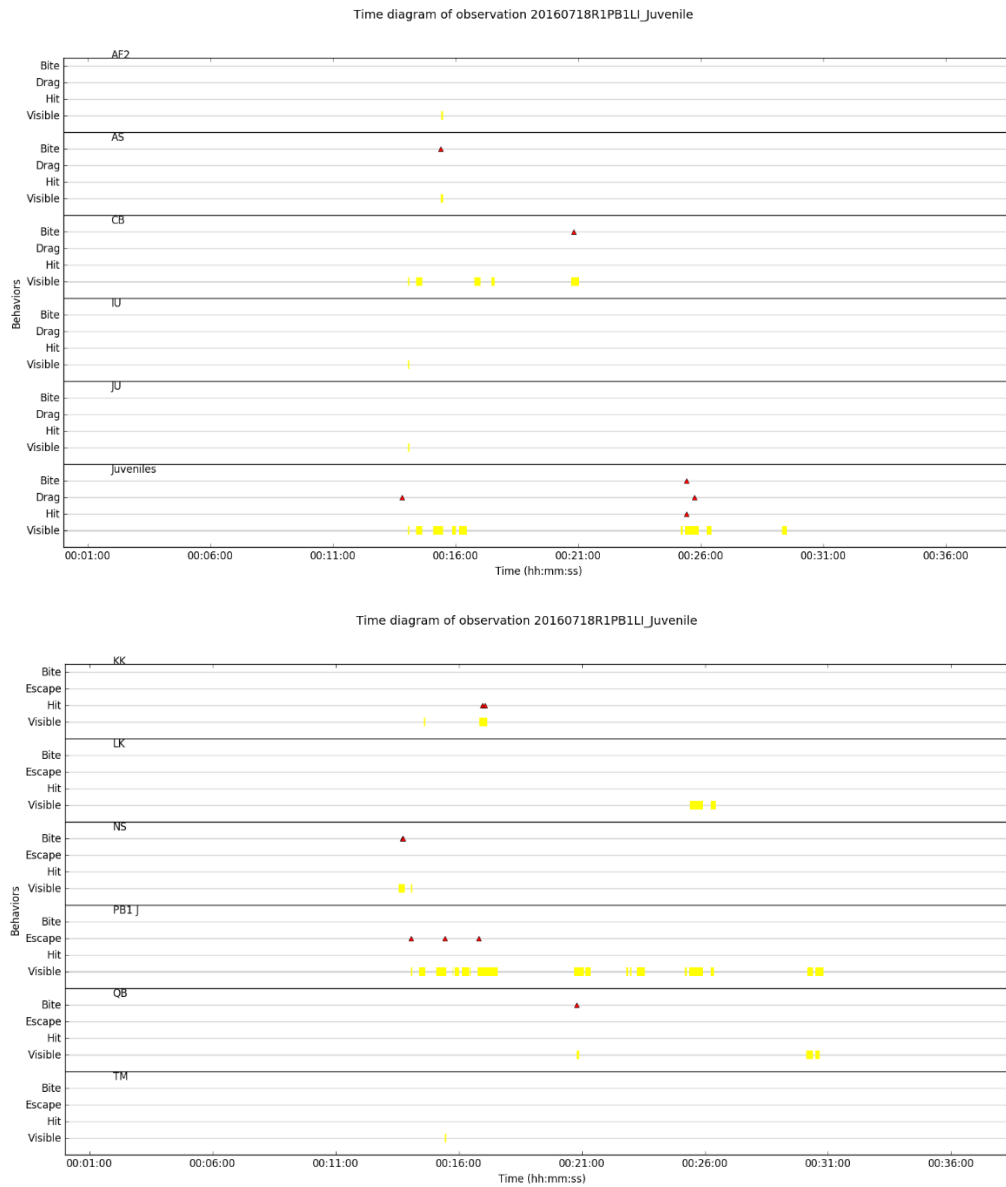


Figure XIII Time-diagrams of the attack on the female juvenile from PB1 by R1 (18th July 2016)

Yams

Summary

Observer: LI**Victim:** Female from PB1 (YS)

The first recordings of this attack were made by JB at 13:20, while she was covering the attack on Gluten. At that point, Yams is up on a rock surrounded by water while Kevin and Lucifer threat her from the other side of the water. Then JB continues with the observation on Gluten. At 13:23, JB records how Yams is surrounded by Gina, Caca and a juvenile. Caca bites her arm while Gina pulls her crest. Yams does not resist. This is the last observation from JB.

While following the events happening to the juvenile of PB1, around 13:30, I (LI) detected 4 juveniles, an adolescent female, Ani and Mowgli around Yams. She was sitting down and apparently paralyzed. Mowgli grabs her forehead and pulls backwards. She does not resist but displays silent bared teeth. He stops and then Ani and a juvenile touch her briefly, after which Ani stays holding her hand. Caca approaches the group while a juvenile observes Yams face intently. Yams teeth-chatter towards Mowgli, whose face is not clearly visible and then Ani grabs the fur of Yam's forehead and pulls backwards. Yams does not struggle and curls up when Ani stops pulling. Then the observation is interrupted to check on the juvenile of PB1. When observing Yams again within the same minute, only Ani and Mowgli are still around her and Yams sits down between them, apparently paralyzed. Shortly after, she seems to recover conscience and looks around, detecting where some members of PB1 are. Then she starts walking towards there with silent-bared teeth. Ani grabs her and forces her to turn her head towards her. Then Ani releases Yams and Yams jumps and flees 13:31. Some juveniles chased her for a few meters but then stop, once she reaches an area where some members of PB1 were (Codot, Mr.I, Fonz).



The first recordings of this attack were made by JB at 13:20, while she was covering the attack on Gluten. At that point, Yams is up on a rock surrounded by water while Kevin and Lucifer threat her from the other side of the water (Figure XIV, Picture 1). Then JB continues with the observation on Gluten. At 13:23, JB records how Yams is surrounded by Gina, Caca and a juvenile. Caca bites her arm while Gina pulls her crest. Yams does not resist(Figure XIV, Picture 2). This is the last observation from JB

While following the events happening to the juvenile of PB1, around 13:30, I (LI) detected 4 juveniles, an adolescent female, Ani and Mowgli around Yams. She was sitting down and apparently paralyzed. Mowgli grabs her forehead and pulls backwards. She does not resist but displays silent bared teeth (Figure XIV, Picture 3). He stops and then Ani and a juvenile touch her briefly, after which Ani stays holding her hand. Caca approaches the group while a juvenile observes Yams face intently. Yams teeth-chatter towards Mowgli, whose face is not clearly visible and then Ani grabs the fur of Yam's forehead and pulls backwards. Yams does not struggle and curls up when Ani stops pulling. Then the observation is interrupted to check on the juvenile of PB1. When observing Yams again within the same minute, only Ani and Mowgli are still around her and Yams sits down between them, apparently paralyzed. Shortly after, she seems to recover conscience and looks around, detecting where some members of PB1 are. Then she starts walking towards there with silent-bared teeth. Ani grabs her and forces her to turn her head towards her. Then Ani releases Yams and Yams jumps and flees 13:31 (Figure XIV, Picture 4) . Some juveniles chased her for a few meters but then stop, once she reaches an area where some members of PB1 were (Codot, Mr.I, Fonz).

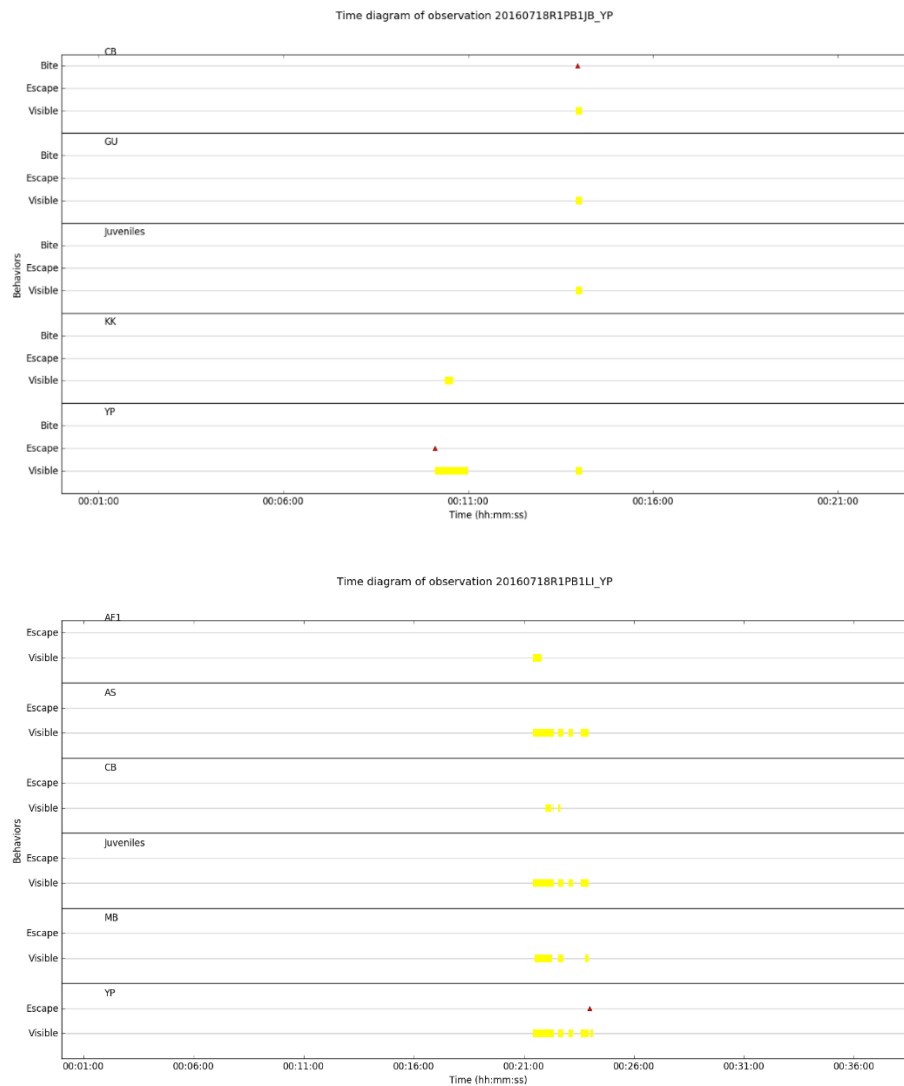


Figure XV Time-diagrams of the attack on YP from PB1 by R1 (18th July 2016)

4.2. Information on the intergroup coalitionary encounters from the back records

3RD AUGUST 2006: AMBER (AD) HARASSED BY R1

Material: 5 pictures taken by Antje Engelhardt during the harassment and personal comments.

One of the pictures (8:07) shows Amber curled up on the ground with two individuals (possibly a juvenile and a female, but their back points toward the camera and cannot be confirmed), sitting next to her. A third one seems to be standing behind her, but only some fingers are visible.

Another picture (8:48) shows the face of Amber during the harassment. She is resting the left side of her face on the ground and her eyes are half open, giving the impression of being dead. She has an injury of a couple of centimeters on the right side of her head (the skin has been removed but is not bleeding)

The third picture (8:50) shows Amber facing down on the ground with three individuals around her (only their arms are visible, but none seems to have adult male size).

In the fourth picture (8:50 as well) Amber is in the same posture as in the third one and with the same number of individuals, but one of them is inspecting her anal area.

In the fifth (8:51), a juvenile male sits by her while Amber lies down on the ground looking dead.

The harassment lasted for about 45 minutes and was carried out by a number of juveniles, females and sub-adults. Amber survived.

18TH JULY 2007: INDA (ID) FROM R2 HARASSED BY R1

Material: 10 pictures, unknown author. Spreadsheet by Teija Febranouva.

The pictures show ID curled up on the ground, apparently protecting her infant. She has a wound on the left side of her mouth, round with a couple of centimeters of diameter. She is surrounded several individuals, including an adult male, juveniles and females. In two of the pictures, an individual is taking ID's chin with its hand making her to look at it. The spreadsheet adds that there was an encounter between R1 and R2, but there are no comments about the attack.

16TH FEBRUARY 2008: HARASSMENT TO ADULT FEMALE WITH INFANT OF NON-HABITUATED GROUP BY R1

Material: 4 non-consecutive videos of a total length of 2 minutes 54 seconds without sound and a spreadsheet. The observer was Teija Febranouva

First video (26.5 seconds): A female with an infant is harassed by a sub-adult male, what seems like 3 juveniles and a female. The sub-adult bites her on the back and the female grabs her. Then the victim flees twice for a few meters but both times is quickly caught by the aggressors. When catching her the second time, a sub-adult jumps on her back and runs away, while the female and another individual bite the victim. When the female aggressor turns around, she has fur on her mouth. A juvenile grabs some of the female's fur from the back. Then the victim runs away again, showing the long cut (~10 cm) that she has on her left flank.

She is caught again by a juvenile and a sub-adult, who presses her against the ground. A juvenile smells her and then grabs her fur and pulls and tries to examine her face, but the sub-adult grabs the victim and pulls her toward him. The sub-adult bites her and another one together with a juvenile examine her. One of the sub-adults grabs fur of her back and pulls and in doing this, the victim tries to run away again. She manages to not being caught up to the end of the video.

Second video (1minute, 19 seconds): The victim is curled up on the ground and a female and a sub-adult manipulate her body, while a juvenile watches. The sub-adult leaves and the juvenile and the female bite the victim. She tries to run away but is trapped by the aggressors. Two juveniles bite her and a third individual touches her back. The juveniles bite her again. Then the female and a juvenile, while a third individual wraps its arm around her. The female bites the victim's arm. Then the sub-adult and a juvenile seem to bite as well. More individuals join the attack and soon is not possible to see who is doing what or even how many they are exactly, but at least seven.

Suddenly, most of the aggressors flee and the victim is left alone on the ground laying down. The sub-adult and a female are still close to her. The female moves away and the sub-adult stays manipulating the victim, rolling her on the ground. The female comes back and grabs the victim's crest and pulls. The sub-adult drags the victim by pulling from an arm. Then he stands on her. When he steps down, the female approaches the victim with 3 juveniles, that start attacking the victim. They manage to turn her upside

down and when they do, they start biting her abdomen violently, particularly the sub-adult. She does not resist at any point. When the aggressors start leaving, the victim manages to lay facing down. Only a small juvenile stays with her; it puts its hand on her head and then jumps away. The victim then turns the head slightly, showing a sizeable wound on the right side of her forehead before she escapes.

Third video (45 seconds): The victim is hidden by a crowd of juveniles, a female and a couple of sub-adults. Some individuals seem to bite her, but is unclear. A female grab's the victim's back and then the victim defecates, while is attacked by juveniles. The female bites her as well. The victim moves slightly, trying to put all her limbs under her body. Then she is turned upside down by her aggressors, showing the long cut on her left flank. Two juveniles bite her and a third individual grabs her crest and drags her towards itself. There is blood on her sexual skin. A couple of juveniles touch and smell her. A juvenile grabs her leg and drag her towards it and then turns her upside down. It and another juvenile bite her. She has blood on her face. She is dragged by a female and when this releases her, the victim flees and is chased by a juvenile and a sub-adult.

Fourth video (25 seconds): An infant walking. I am not sure whether is related to the previous one or not since the date of capture is not available.

Comment in spreadsheet: *"1 female with infant caught and being harrassed by Ff and Jj R1. {BS,TS,QS HS etc}. the female escaped wt so many injured while the infant lefted in R1. carried by R1 adolescent female."*

16TH JUNE 2008: R1 HARASSING AN INFANT FROM R2

Material: 2 entries on the long term data base of individual events (Table II) plus confirmation (email communication) with one of the observers (Julie Dubosq).

According to one of the observers (Julie Duboscq), GD's infant (male), from R2, was isolated during an intergroup encounter between R1 and R2. It was harassed by several females and juveniles. His mother, GD (Ginger), was chased by an adult male (FJ, Barra). Both, mother and infant returned to their group, but the infant was severely injured on his head and died 5 days after the attack.

Table II The 2 entries of the demography long term database of the MNP referencing an intergroup coalitionary attack

ID	GD	GD1B
name	Ginger	--
sex	f	male
group	R2	R2
date	16/06/2008	21/06/2008
event	infant injury	death
detail 1	GD1B	
detail 2	head	injuries to head
detail 3	intergroup encounter	
detail 4	R1, R2	
observers	JD, ML	AN
notes	Pos3; harassed by juveniles, females; GD harassed by FJ	

2ND NOVEMBER 2008: R1 HARASSING A JUVENILE OF EITHER R2 OR R3 (TRIADIC ENCOUNTER)

Material: 4 pictures and spreadsheet by Jerome Michelleta

Three of the pictures show the juvenile curled up on the ground surrounded by juveniles, sub-adults-females and adolescents, with some of the juveniles touching the victim. In two of them there is a male seating about a meter away from the victim. The fourth picture shows the juvenile being examined by 2 individuals, possibly juveniles or sub-adults, while it is laying down on its abdomen. The comment in the spreadsheet was: *"1j R2/3? harassed bleeding when escaped"*

4.3. Rscript with results: Non-orthogonal planed contrasts in Poisson GLMM to investigate whether age-sex classes differ in their participation in IGCAs

```
## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("DHARMa")#Residual Diagnostics for Hierarchical (Multi-Level / Mixed) Regression
Models
install.packages("ggeffects")
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
```

```
library(lme4)
library(car)
library(ggplot2)
library(MuMIn)
library(DHARMa)
library(ggeffects)
library(sjPlot)
```

```
#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/_PostViva_Revision/Revision_Ch4")
getwd()
```

```
## Upload data
```

```
data<-read.csv("Chapter4_revision_database.csv")
```

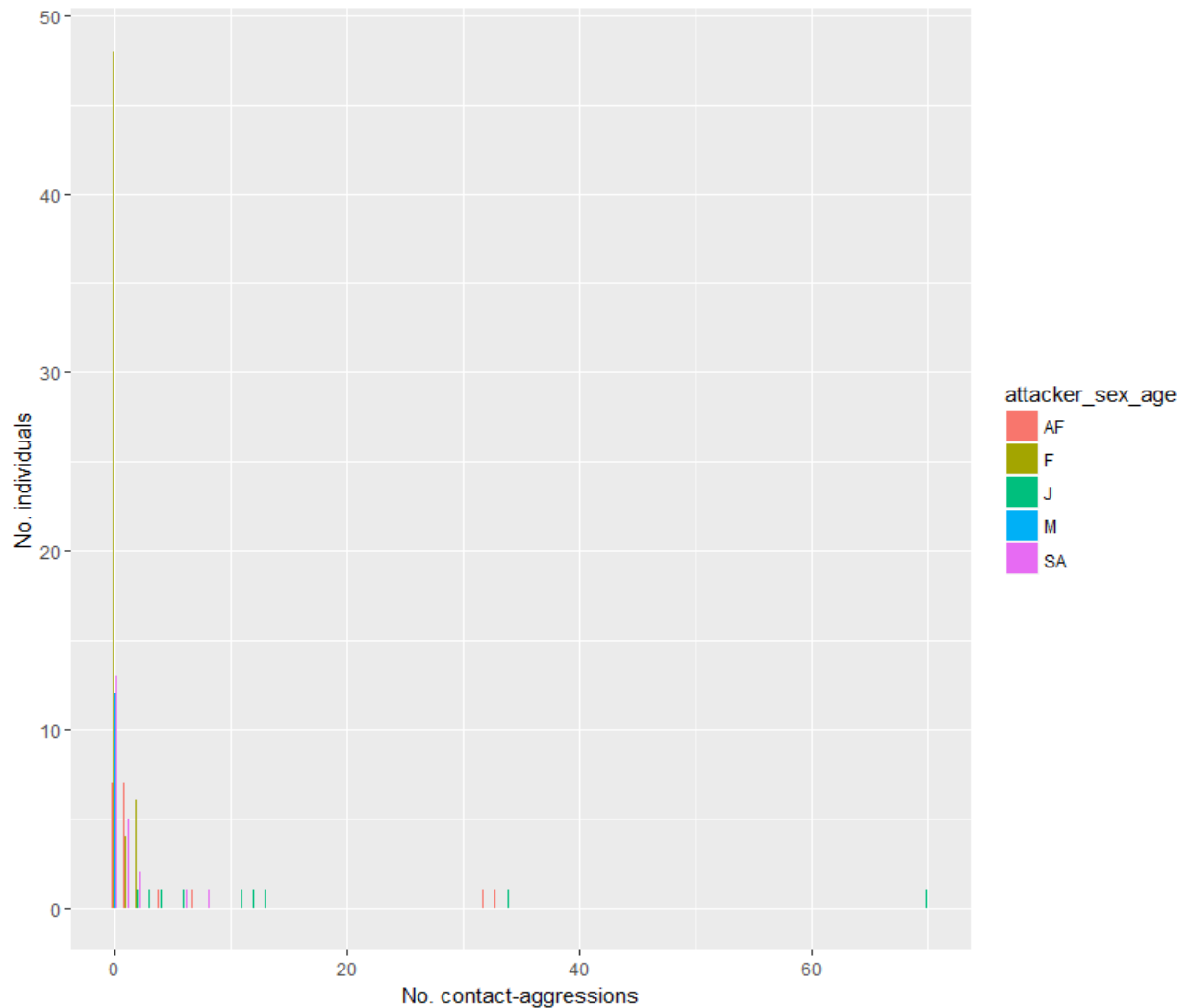
```
head(data)
```

```
#Preparing the variables
data$N_bites<- as.numeric(data$N_bites)
data$N_drag<- as.numeric(data$N_drag)
data$N_N_pull<- as.numeric(data$N_pull)
data$N_hit<- as.numeric(data$N_hit)
data$N_caggression<- as.numeric(data$N_caggression)
data$minutes_visible<- as.numeric(data$minutes_visible)
data$bitting_rate<- as.numeric(data$bitting_rate)
data$cag_rate<- as.numeric(data$cag_rate)
data$attack<- factor(data$attack)
data$AttackerID<- factor(data$AttackerID)
```

```

data$attacker_sex_age<- factor(data$attacker_sex_age)
data$attacker_sex<- factor(data$attacker_sex)
> ggplot(data, aes(N_caggression, fill = attacker_sex_age)) +
+   geom_histogram(binwidth=.5, position="dodge")+
+   xlab("No. contact-aggressions")+ylab("No. individuals")

```



```

>
> #Having a look to the different attacks per age-sex class
> tapply(data$N_bites, data$attacker_sex_age, sum)
  AF  F  J  M  SA
 73 13 141 0 19
> tapply(data$N_pull, data$attacker_sex_age, sum)
  AF  F  J  M  SA
  2  0  0  0  0
> tapply(data$N_drag, data$attacker_sex_age, sum)
  AF  F  J  M  SA
  8  3 13  0  1
> tapply(data$N_hit, data$attacker_sex_age, sum)
  AF  F  J  M  SA
  0  0  1  0  3
> tapply(data$N_caggression, data$attacker_sex_age, sum)
  AF  F  J  M  SA
 83 16 155  0 23

```

```
>
```

```
> cat("\n\n\n\n\n\n\n Non-orthogonal planned contrast in Poisson GLMM\n\n\n\n\n\n\n")
```

```
\n
Non-orthogonal planned contrast in Poisson GLMM
```

```
>
> table(data$attacker_sex_age)

AF  F  J  M SA
18 58 11 12 22
>
> #Eliminate juveniles that couldn't be individually ID
> data<-data[data$AttackerID!="J",]
> table(data$attacker_sex_age)

AF  F  J  M SA
18 58  3 12 22
>
> # The R-formula should thus look something like:
> # n bites~ Age-sex class + offset(log(n minutes within 2m) + (1|IGCA event/attacker ID), family= "poisson"
> #offset: An offset is a term to be added to a linear predictor, such as
in a generalised linear model, with known coefficient
> # 1 rather than an estimated coefficient.Best explained in : https://www.youtube.com/watch?v=3Jbaxp3whDA 7
> # and https://www.mbaskool.com/business-concepts/statistics/7554-offset.html
>
>
>
> levels(data$attacker_sex_age)
[1] "AF" "F"  "J"  "M"  "SA"
> contrasts(data$attacker_sex_age)
      F J M SA
AF 0 0 0 0
F  1 0 0 0
J  0 1 0 0
M  0 0 1 0
SA 0 0 0 1
>
> contrasts(data$attacker_sex_age)<- cbind(Female.vs.Male= c(1.5,1.5,-1,-1,-1),
+                                         Adult.vs.Immature= c(-1,1.5,-1,1.5,-1),
+                                         AdultFemale.vs.Adol.Female= c(-1, 1, 0, 0, 0),
+                                         Adult.Male.vs.SubAd.male= c(0, 0, 0, 1, -1))
> contrasts(data$attacker_sex_age)
      Female.vs.Male Adult.vs.Immature AdultFemale.vs.Adol.Female Adult.Male.vs.SubAd.male
AF              1.5             -1.0                -1                0
F               1.5              1.5                 1                0
J              -1.0             -1.0                 0                0
M              -1.0              1.5                 0                1
```



```

SA          -1.0          -1.0          0          -1
>
> mod<-glmer(N_caggression~attacker_sex_age+offset(log(minutes_visible))+(
1|attack/AttackerID), family="poisson", data=data)
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
  Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
>
> summary(mod)
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: poisson ( log )
Formula: N_caggression ~ attacker_sex_age + offset(log(minutes_visible)) +
(1 | attack/AttackerID)
Data: data

      AIC      BIC    logLik deviance df.resid
  243.4    262.5   -114.7    229.4     106

Scaled residuals:
      Min       1Q   Median       3Q      Max
-0.9266 -0.3817 -0.1600  0.0000  3.3219

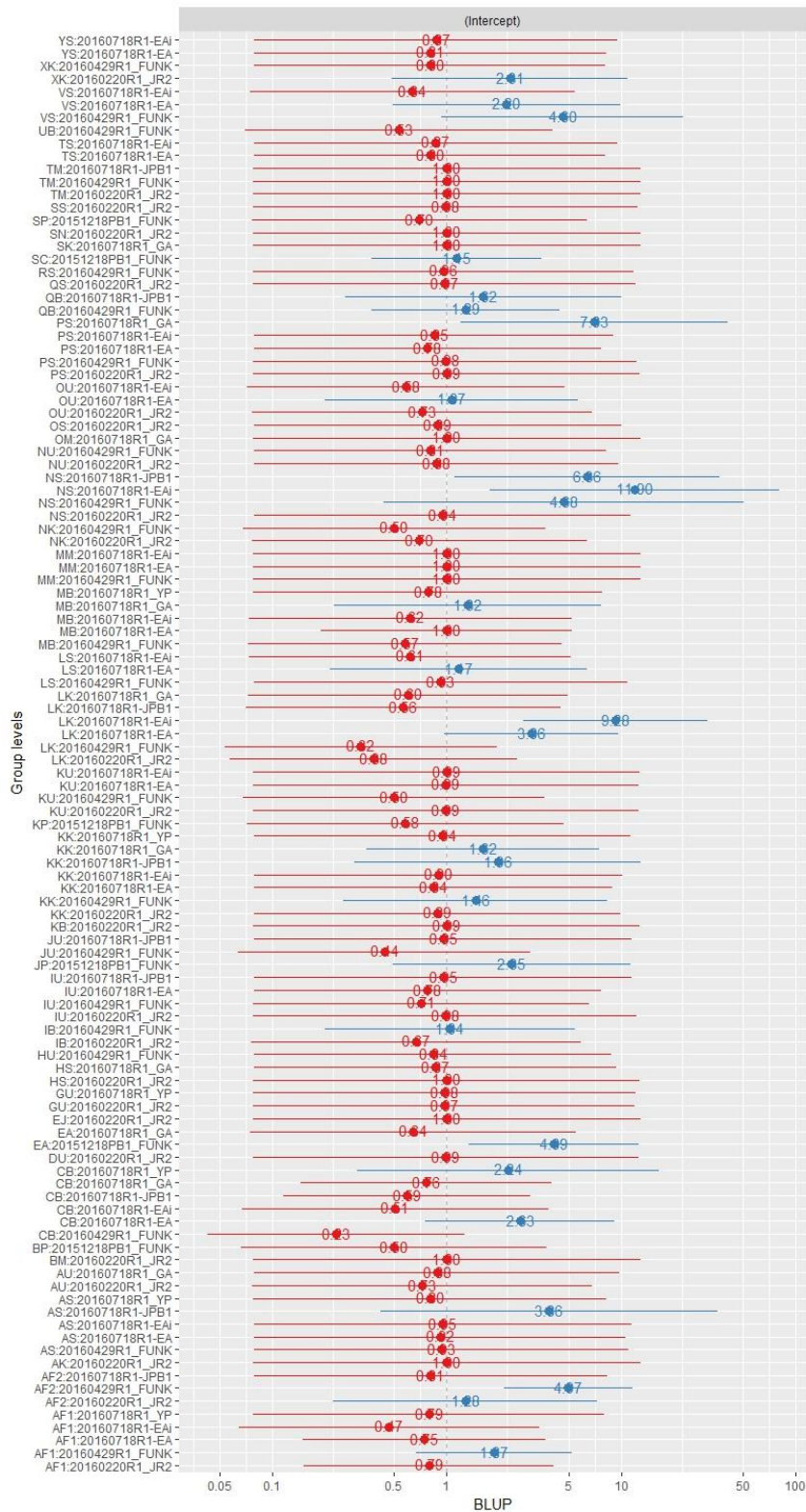
Random effects:
Groups              Name          Variance Std.Dev.
AttackerID:attack (Intercept)  1.6981    1.3031
attack            (Intercept)  0.9523    0.9759
Number of obs: 113, groups: AttackerID:attack, 112; attack, 8

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)      -4.858    231.891  -0.021   0.9833
attacker_sex_ageFemale.vs.Male      3.546    231.891   0.015   0.9878
attacker_sex_ageAdult.vs.Immature   -8.370    463.781  -0.018   0.9856
attacker_sex_ageAdultFemale.vs.Adol.Female    9.701    579.726   0.017   0.9866
attacker_sex_ageAdult.Male.vs.SubAd.male     1.843     1.064   1.732   0.0833 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
      (Intr) a__F.. a__A.. a__AF.
attck__F..M -1.000
attck__A..I  1.000 -1.000
at__AF..A.F -1.000  1.000 -1.000
a__A.M..SA.  0.002 -0.001  0.000  0.000
convergence code: 0
Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?

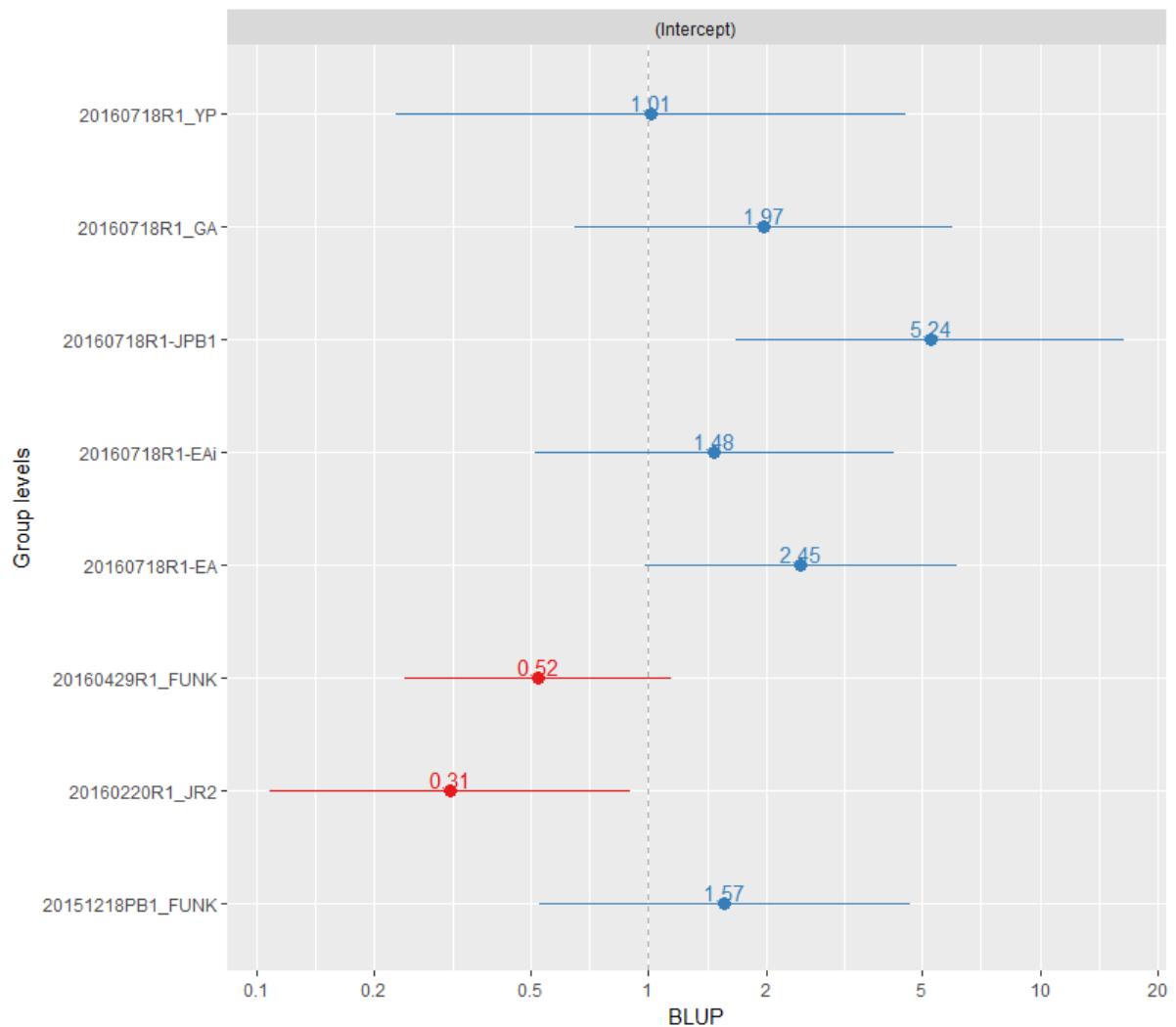
```

```
> #Plot random effects
> sjp.glmer(mod, type = "re", vars = NULL)
Plotting random effects...
```



Plotting random effects...

>



```
> cat("\n\n Checking model assumptions \n\n")
```

Checking model assumptions n

>

```
> #Overdispersion?
```

```
> sim_res<-simulateResiduals(mod, n = 250, refit = F, integerResponse = NU  
LL, plot = F, seed = 123)
```

```
> testDispersion(sim_res, alternative ="greater", plot = T)
```

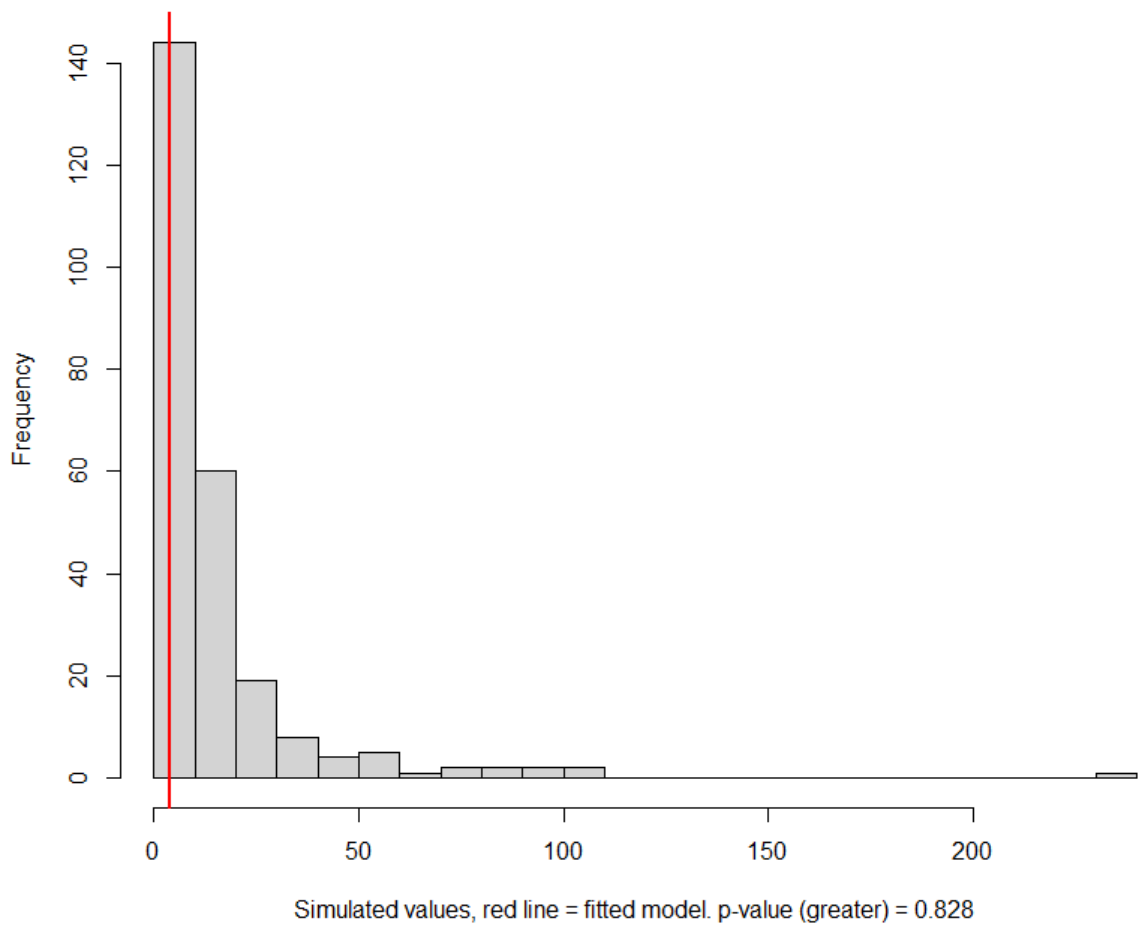
DHARMA nonparametric dispersion test via sd of residuals fitted vs.
simulated

data: simulationOutput

ratioObsSim = 0.2513, p-value = 0.828

alternative hypothesis: greater

DHARMA nonparametric dispersion test via sd of residuals fitted vs. simulated

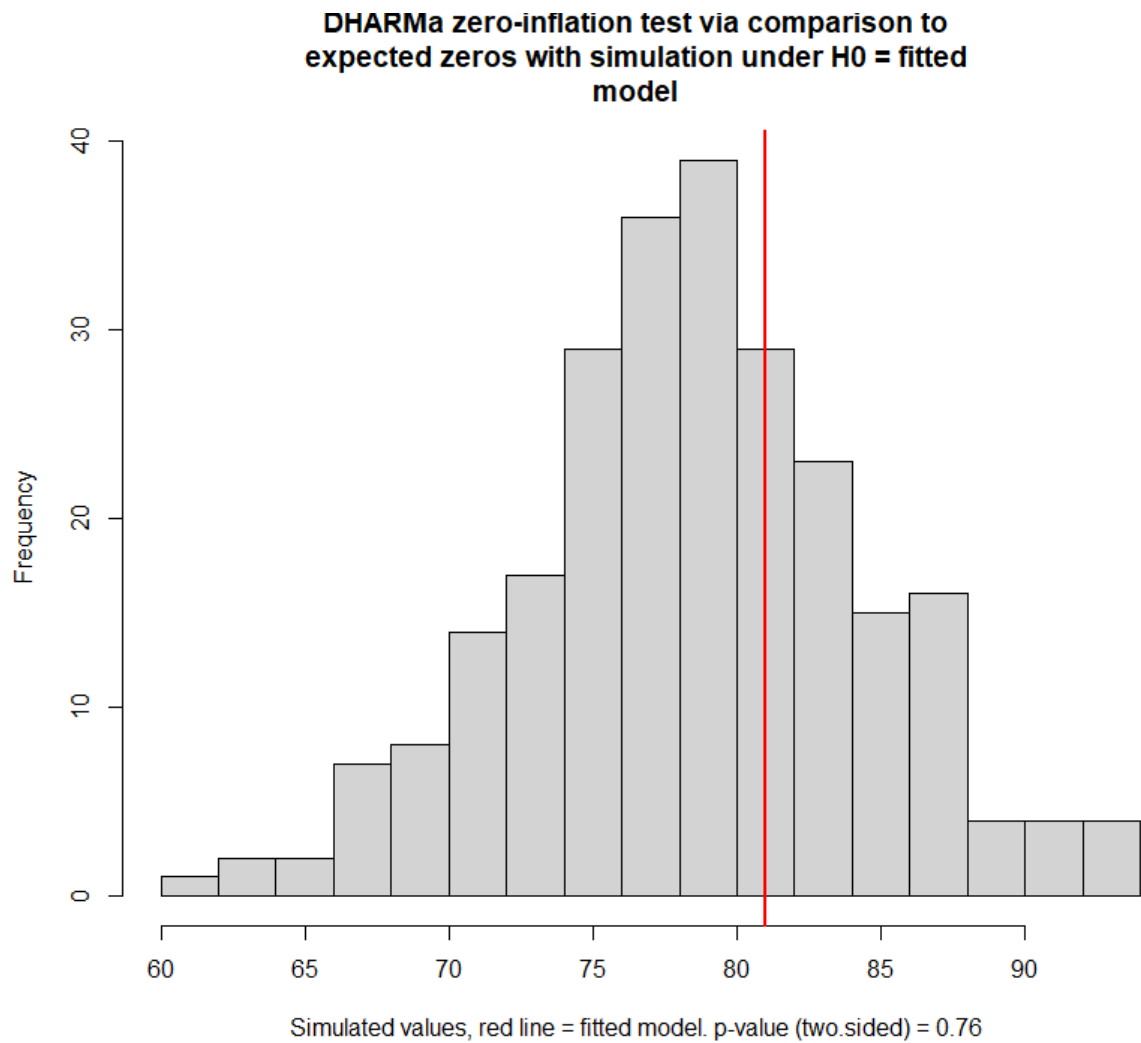


```
> #Zero-inflated?
> testZeroInflation(sim_res, plot = T)
```

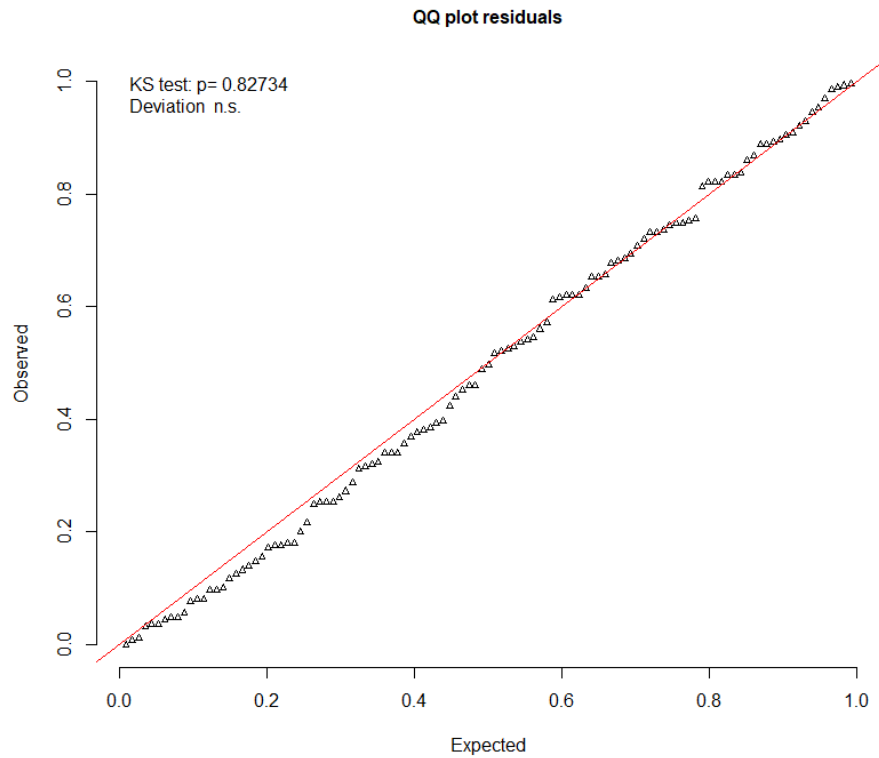
DHARMA zero-inflation test via comparison to expected zeros with simulation under H_0 = fitted model

```
data: simulationOutput
ratioObsSim = 1.0255, p-value = 0.76
alternative hypothesis: two.sided
```

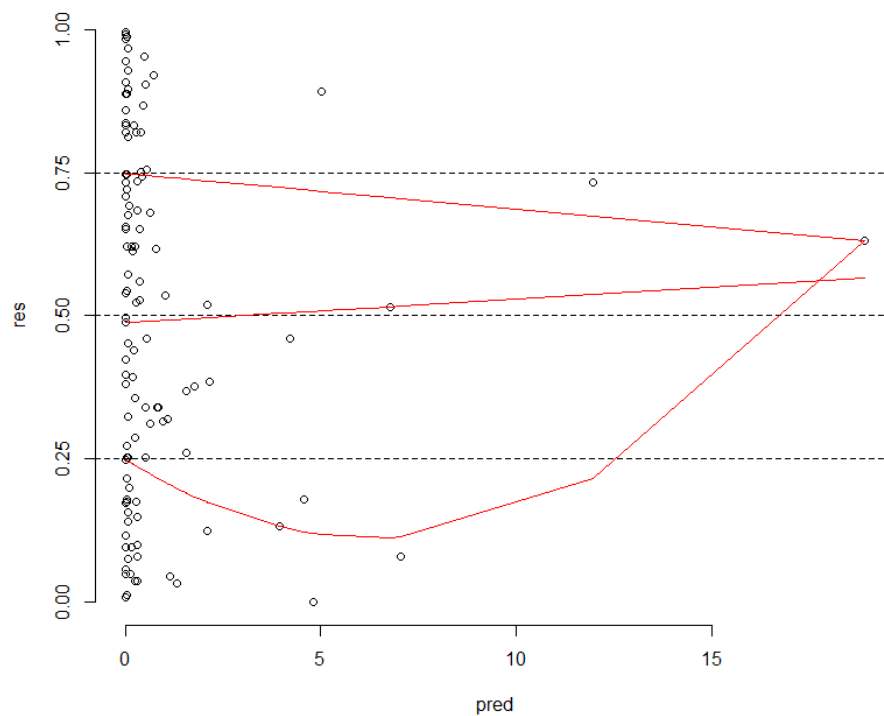
```
> # No according to this
```



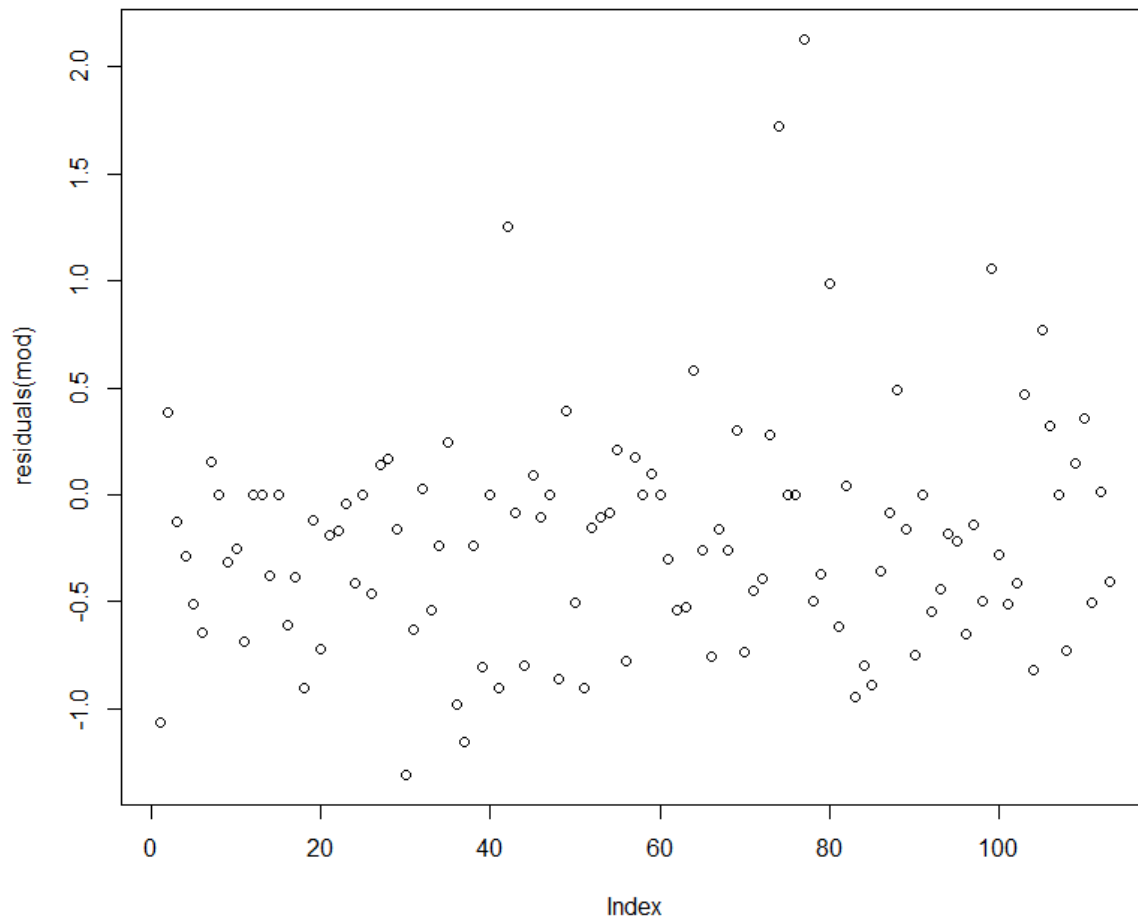
```
> #Checking the residuals  
> plotQQunif(sim_res)
```



```
> #Desviation not significant according to KS test (p=0.8)
> plotResiduals(sim_res)
```



```
> plot(residuals(mod))
```



```
> #Checking cook's distances
>
> plot(cooks.distance(mod))#Cannot be implemented in glmm so an error is p
roduced!
Error in UseMethod("cooks.distance") :
  no applicable method for 'cooks.distance' applied to an object of class
  "c('glmerMod', 'merMod')"
> mod_glm<-glm(N_caggression~attacker_sex_age+offset(log(minutes_visible))
, family="poisson", data=data)
> summary(mod_glm)#Residual deviance: 247.16 on 108 degrees of freedom--
> This would suggest over dispersion (Residual variance>degrees of freedom
)
```

```
Call:
glm(formula = N_caggression ~ attacker_sex_age + offset(log(minutes_visibl
e)),
    family = "poisson", data = data)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-5.0601  -0.8492  -0.3473  -0.0001   6.1002
```

```
Coefficients:
                                Estimate Std. Error z value Pr(
>|z|)
```

```

(Intercept)                -4.3740    220.5966   -0.020
0.984
attacker_sex_ageFemale.vs.Male    3.4793    220.5966    0.016
0.987
attacker_sex_ageAdult.vs.Immature -8.2445    441.1931   -0.019
0.985
attacker_sex_ageAdultFemale.vs.Adol.Female  9.3641    551.4914    0.017
0.986
attacker_sex_ageAdult.Male.vs.SubAd.male    2.0513      0.2655    7.725 1.1
1e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

(Dispersion parameter for poisson family taken to be 1)

```

Null deviance: 419.76  on 112  degrees of freedom
Residual deviance: 275.09  on 108  degrees of freedom
AIC: 371.67

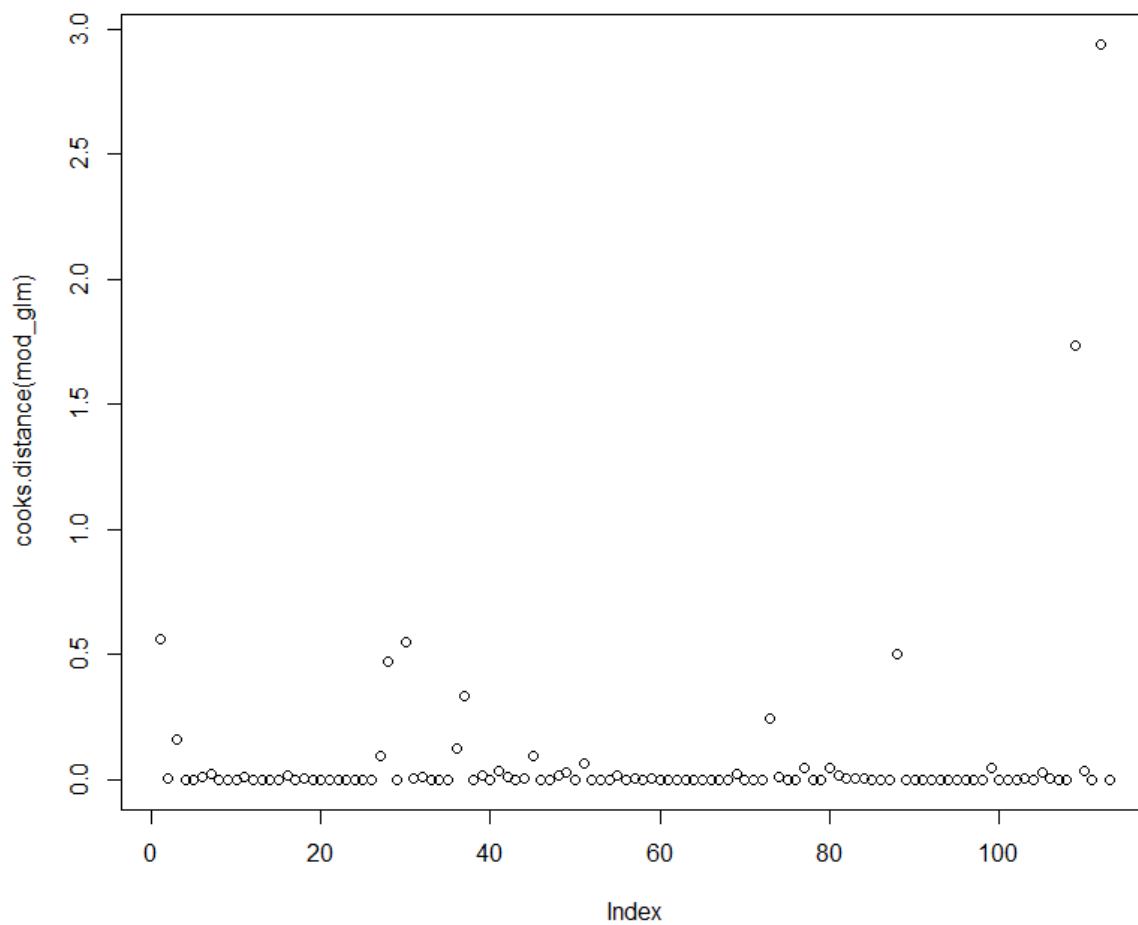
```

Number of Fisher Scoring iterations: 16

```

> plot(cooks.distance(mod_glm))
>

```



```

> check<-data.frame(data$AttackerID,data$attack)
> check$cooks_distance<-cooks.distance(mod_glm)

```



```
> check
```

	data.AttackerID	data.attack	cooks_distance
1	LK	20160220R1_JR2	5.607817e-01
2	XK	20160220R1_JR2	3.972139e-03
3	AF1	20160220R1_JR2	1.588207e-01
4	AS	20160429R1_FUNK	1.413579e-04
5	AS	20160718R1_YP	5.246681e-04
6	NK	20160220R1_JR2	1.371011e-02
7	AF2	20160220R1_JR2	2.224269e-02
8	SN	20160220R1_JR2	1.492838e-09
9	AS	20160718R1-EA	1.028761e-05
10	AS	20160718R1-EAi	1.028761e-05
11	IB	20160220R1_JR2	1.083931e-02
12	BM	20160220R1_JR2	7.457469e-10
13	TM	20160220R1_JR2	4.557434e-10
14	KK	20160220R1_JR2	8.975808e-04
15	EJ	20160220R1_JR2	2.201089e-10
16	AU	20160220R1_JR2	1.580133e-02
17	AU	20160718R1_GA	3.629388e-05
18	BP	20151218PB1_FUNK	5.940599e-03
19	DU	20160220R1_JR2	1.028623e-05
20	EA	20160718R1_GA	8.955295e-04
21	GU	20160220R1_JR2	7.101179e-05
22	GU	20160718R1_YP	4.502745e-06
23	HS	20160220R1_JR2	1.858871e-07
24	HS	20160718R1_GA	5.064593e-05
25	AK	20160220R1_JR2	6.835150e-13
26	HU	20160429R1_FUNK	1.216172e-03
27	AF1	20160429R1_FUNK	9.323710e-02
28	AF2	20160429R1_FUNK	4.709319e-01
29	IU	20160220R1_JR2	3.511220e-05
30	CB	20160429R1_FUNK	5.521234e-01
31	IU	20160429R1_FUNK	6.351602e-03
32	IB	20160429R1_FUNK	1.305334e-02
33	IU	20160718R1-EA	1.212040e-04
34	IU	20160718R1-JPB1	6.622237e-07
35	KK	20160429R1_FUNK	6.766275e-04
36	JU	20160429R1_FUNK	1.258663e-01
37	LK	20160429R1_FUNK	3.357074e-01
38	JU	20160718R1-JPB1	6.622237e-07
39	MB	20160429R1_FUNK	1.635041e-02
40	MM	20160429R1_FUNK	1.277688e-08
41	NK	20160429R1_FUNK	3.836310e-02
42	AS	20160718R1-JPB1	1.220038e-02
43	KB	20160220R1_JR2	2.755624e-06
44	KP	20151218PB1_FUNK	2.669778e-03
45	QB	20160429R1_FUNK	9.457973e-02
46	KU	20160220R1_JR2	5.842784e-06
47	TM	20160429R1_FUNK	4.278622e-09
48	UB	20160429R1_FUNK	1.466705e-02
49	JP	20151218PB1_FUNK	2.943431e-02
50	XK	20160429R1_FUNK	1.309266e-03
51	KU	20160429R1_FUNK	6.477035e-02
52	CB	20160718R1_GA	4.041206e-04
53	KU	20160718R1-EA	1.154447e-07
54	KU	20160718R1-EAi	1.154447e-07
55	KK	20160718R1_GA	1.636647e-02
56	LK	20160718R1_GA	8.932362e-04
57	MB	20160718R1_GA	3.250186e-03
58	OM	20160718R1_GA	7.091543e-12

59	LS	20160718R1-EA	4.725957e-03
60	SK	20160718R1_GA	2.431416e-11
61	LS	20160429R1_FUNK	1.769070e-04
62	MB	20160718R1_YP	4.641676e-04
63	AF1	20160718R1_YP	2.399882e-04
64	CB	20160718R1_YP	8.235886e-04
65	KK	20160718R1_YP	1.679817e-05
66	LS	20160718R1-EAi	2.109411e-03
67	AF1	20160718R1-EA	6.983858e-05
68	NS	20160220R1_JR2	2.776872e-04
69	CB	20160718R1-EA	2.268252e-02
70	NS	20160718R1-EAi	4.786586e-06
71	KK	20160718R1-EA	3.237242e-05
72	NU	20160220R1_JR2	1.731384e-03
73	LK	20160718R1-EA	2.461060e-01
74	NS	20160429R1_FUNK	1.140922e-02
75	MB	20160718R1-EA	2.179933e-03
76	MM	20160718R1-EA	7.170949e-11
77	NS	20160718R1-EAi	4.914754e-02
78	NU	20160429R1_FUNK	1.861934e-03
79	OS	20160220R1_JR2	1.294603e-03
80	NS	20160718R1-JPB1	4.849731e-02
81	OU	20160220R1_JR2	1.602330e-02
82	OU	20160718R1-EA	3.770831e-03
83	AF1	20160718R1-EAi	3.380907e-03
84	OU	20160718R1-EAi	2.889714e-03
85	CB	20160718R1-EAi	2.309889e-03
86	KK	20160718R1-EAi	3.237242e-05
87	PS	20160220R1_JR2	2.486005e-06
88	LK	20160718R1-EAi	5.014336e-01
89	PS	20160429R1_FUNK	1.282723e-05
90	MB	20160718R1-EAi	1.311921e-03
91	MM	20160718R1-EAi	7.170949e-11
92	PS	20160718R1-EA	1.228808e-04
93	PS	20160718R1-EAi	1.228808e-04
94	QS	20160220R1_JR2	6.355380e-05
95	RS	20160429R1_FUNK	4.581397e-05
96	SP	20151218PB1_FUNK	7.735906e-04
97	SS	20160220R1_JR2	1.953811e-05
98	AF2	20160718R1-JPB1	6.878761e-06
99	PS	20160718R1_GA	4.663512e-02
100	CB	20160718R1-JPB1	1.358590e-04
101	TS	20160718R1-EA	8.939883e-05
102	TS	20160718R1-EAi	8.939883e-05
103	KK	20160718R1-JPB1	7.525254e-03
104	LK	20160718R1-JPB1	1.749752e-04
105	VS	20160429R1_FUNK	2.715817e-02
106	QB	20160718R1-JPB1	7.041421e-03
107	TM	20160718R1-JPB1	2.973461e-13
108	VS	20160718R1-EAi	1.701153e-03
109	EA	20151218PB1_FUNK	1.736056e+00
110	VS	20160718R1-EA	3.516277e-02
111	YS	20160718R1-EA	8.319649e-05
112	SC	20151218PB1_FUNK	2.939784e+00
113	YS	20160718R1-EAi	8.319649e-05

> # Models with distances over 1 are said to be influential (eg. Field et al 2012) or 4/N (which in this case would be 0.035)

> check\$large.cooks.distance<- check\$cooks_distance > 1

> check

data.AttackerID data.attack cooks_distance large.cooks.distance

1	LK	20160220R1_JR2	5.607817e-01	FALSE
2	XK	20160220R1_JR2	3.972139e-03	FALSE
3	AF1	20160220R1_JR2	1.588207e-01	FALSE
4	AS	20160429R1_FUNK	1.413579e-04	FALSE
5	AS	20160718R1_YP	5.246681e-04	FALSE
6	NK	20160220R1_JR2	1.371011e-02	FALSE
7	AF2	20160220R1_JR2	2.224269e-02	FALSE
8	SN	20160220R1_JR2	1.492838e-09	FALSE
9	AS	20160718R1-EA	1.028761e-05	FALSE
10	AS	20160718R1-EAi	1.028761e-05	FALSE
11	IB	20160220R1_JR2	1.083931e-02	FALSE
12	BM	20160220R1_JR2	7.457469e-10	FALSE
13	TM	20160220R1_JR2	4.557434e-10	FALSE
14	KK	20160220R1_JR2	8.975808e-04	FALSE
15	EJ	20160220R1_JR2	2.201089e-10	FALSE
16	AU	20160220R1_JR2	1.580133e-02	FALSE
17	AU	20160718R1_GA	3.629388e-05	FALSE
18	BP	20151218PB1_FUNK	5.940599e-03	FALSE
19	DU	20160220R1_JR2	1.028623e-05	FALSE
20	EA	20160718R1_GA	8.955295e-04	FALSE
21	GU	20160220R1_JR2	7.101179e-05	FALSE
22	GU	20160718R1_YP	4.502745e-06	FALSE
23	HS	20160220R1_JR2	1.858871e-07	FALSE
24	HS	20160718R1_GA	5.064593e-05	FALSE
25	AK	20160220R1_JR2	6.835150e-13	FALSE
26	HU	20160429R1_FUNK	1.216172e-03	FALSE
27	AF1	20160429R1_FUNK	9.323710e-02	FALSE
28	AF2	20160429R1_FUNK	4.709319e-01	FALSE
29	IU	20160220R1_JR2	3.511220e-05	FALSE
30	CB	20160429R1_FUNK	5.521234e-01	FALSE
31	IU	20160429R1_FUNK	6.351602e-03	FALSE
32	IB	20160429R1_FUNK	1.305334e-02	FALSE
33	IU	20160718R1-EA	1.212040e-04	FALSE
34	IU	20160718R1-JPB1	6.622237e-07	FALSE
35	KK	20160429R1_FUNK	6.766275e-04	FALSE
36	JU	20160429R1_FUNK	1.258663e-01	FALSE
37	LK	20160429R1_FUNK	3.357074e-01	FALSE
38	JU	20160718R1-JPB1	6.622237e-07	FALSE
39	MB	20160429R1_FUNK	1.635041e-02	FALSE
40	MM	20160429R1_FUNK	1.277688e-08	FALSE
41	NK	20160429R1_FUNK	3.836310e-02	FALSE
42	AS	20160718R1-JPB1	1.220038e-02	FALSE
43	KB	20160220R1_JR2	2.755624e-06	FALSE
44	KP	20151218PB1_FUNK	2.669778e-03	FALSE
45	QB	20160429R1_FUNK	9.457973e-02	FALSE
46	KU	20160220R1_JR2	5.842784e-06	FALSE
47	TM	20160429R1_FUNK	4.278622e-09	FALSE
48	UB	20160429R1_FUNK	1.466705e-02	FALSE
49	JP	20151218PB1_FUNK	2.943431e-02	FALSE
50	XK	20160429R1_FUNK	1.309266e-03	FALSE
51	KU	20160429R1_FUNK	6.477035e-02	FALSE
52	CB	20160718R1_GA	4.041206e-04	FALSE
53	KU	20160718R1-EA	1.154447e-07	FALSE
54	KU	20160718R1-EAi	1.154447e-07	FALSE
55	KK	20160718R1_GA	1.636647e-02	FALSE
56	LK	20160718R1_GA	8.932362e-04	FALSE
57	MB	20160718R1_GA	3.250186e-03	FALSE
58	OM	20160718R1_GA	7.091543e-12	FALSE
59	LS	20160718R1-EA	4.725957e-03	FALSE
60	SK	20160718R1_GA	2.431416e-11	FALSE

61	LS	20160429R1_FUNK	1.769070e-04	FALSE
62	MB	20160718R1_YP	4.641676e-04	FALSE
63	AF1	20160718R1_YP	2.399882e-04	FALSE
64	CB	20160718R1_YP	8.235886e-04	FALSE
65	KK	20160718R1_YP	1.679817e-05	FALSE
66	LS	20160718R1-EAi	2.109411e-03	FALSE
67	AF1	20160718R1-EA	6.983858e-05	FALSE
68	NS	20160220R1_JR2	2.776872e-04	FALSE
69	CB	20160718R1-EA	2.268252e-02	FALSE
70	NS	20160718R1-EAi	4.786586e-06	FALSE
71	KK	20160718R1-EA	3.237242e-05	FALSE
72	NU	20160220R1_JR2	1.731384e-03	FALSE
73	LK	20160718R1-EA	2.461060e-01	FALSE
74	NS	20160429R1_FUNK	1.140922e-02	FALSE
75	MB	20160718R1-EA	2.179933e-03	FALSE
76	MM	20160718R1-EA	7.170949e-11	FALSE
77	NS	20160718R1-EAi	4.914754e-02	FALSE
78	NU	20160429R1_FUNK	1.861934e-03	FALSE
79	OS	20160220R1_JR2	1.294603e-03	FALSE
80	NS	20160718R1-JPB1	4.849731e-02	FALSE
81	OU	20160220R1_JR2	1.602330e-02	FALSE
82	OU	20160718R1-EA	3.770831e-03	FALSE
83	AF1	20160718R1-EAi	3.380907e-03	FALSE
84	OU	20160718R1-EAi	2.889714e-03	FALSE
85	CB	20160718R1-EAi	2.309889e-03	FALSE
86	KK	20160718R1-EAi	3.237242e-05	FALSE
87	PS	20160220R1_JR2	2.486005e-06	FALSE
88	LK	20160718R1-EAi	5.014336e-01	FALSE
89	PS	20160429R1_FUNK	1.282723e-05	FALSE
90	MB	20160718R1-EAi	1.311921e-03	FALSE
91	MM	20160718R1-EAi	7.170949e-11	FALSE
92	PS	20160718R1-EA	1.228808e-04	FALSE
93	PS	20160718R1-EAi	1.228808e-04	FALSE
94	QS	20160220R1_JR2	6.355380e-05	FALSE
95	RS	20160429R1_FUNK	4.581397e-05	FALSE
96	SP	20151218PB1_FUNK	7.735906e-04	FALSE
97	SS	20160220R1_JR2	1.953811e-05	FALSE
98	AF2	20160718R1-JPB1	6.878761e-06	FALSE
99	PS	20160718R1_GA	4.663512e-02	FALSE
100	CB	20160718R1-JPB1	1.358590e-04	FALSE
101	TS	20160718R1-EA	8.939883e-05	FALSE
102	TS	20160718R1-EAi	8.939883e-05	FALSE
103	KK	20160718R1-JPB1	7.525254e-03	FALSE
104	LK	20160718R1-JPB1	1.749752e-04	FALSE
105	VS	20160429R1_FUNK	2.715817e-02	FALSE
106	QB	20160718R1-JPB1	7.041421e-03	FALSE
107	TM	20160718R1-JPB1	2.973461e-13	FALSE
108	VS	20160718R1-EAi	1.701153e-03	FALSE
109	EA	20151218PB1_FUNK	1.736056e+00	TRUE
110	VS	20160718R1-EA	3.516277e-02	FALSE
111	YS	20160718R1-EA	8.319649e-05	FALSE
112	SC	20151218PB1_FUNK	2.939784e+00	TRUE
113	YS	20160718R1-EAi	8.319649e-05	FALSE

```
> #The observations with high influence (cook distance>1) are Emping and S
ashimi in the attack that ended in death
> #If we wanted to remove them, the model them would be as follows
> table(data$attacker_sex_age)
```

```
AF  F  J  M  SA
18 58  3 12 22
```

```

> str(data)#113 observations
'data.frame': 113 obs. of 20 variables:
 $ attack      : Factor w/ 8 levels "20151218PB1_FUNK",...: 2 2 2 3 8 2
 2 2 4 5 ...
 $ attacker_group : Factor w/ 2 levels "PB1","R1": 2 2 2 2 2 2 2 2 2 2 ..
.
 $ victim_sex_age : Factor w/ 5 levels "AF","F","I","J",...: 5 5 5 2 2 5 5
 5 2 3 ...
 $ victims_sex    : Factor w/ 2 levels "F","UNK": 1 1 1 1 1 1 1 1 1 1 ...
 $ victim_group   : Factor w/ 3 levels "PB1","R2","UNK": 2 2 2 3 1 2 2 2
 1 1 ...
 $ Victim_ID      : Factor w/ 8 levels "EA","Eai","FUNK1",...: 7 7 7 4 8 7
 7 7 1 2 ...
 $ AttackerID     : Factor w/ 48 levels "AF1","AF2","AK",...: 24 47 1 4 4
 28 2 40 4 4 ...
 $ attacker_sex_age: Factor w/ 5 levels "AF","F","J","M",...: 5 5 1 2 2 5 1
 4 2 2 ...
 ..- attr(*, "contrasts")= num [1:5, 1:4] 1.5 1.5 -1 -1 -1 -1 1.5 -1 1.5
 -1 ...
 .. ..- attr(*, "dimnames")=List of 2
 .. .. $ : chr "AF" "F" "J" "M" ...
 .. .. $ : chr "Female.vs.Male" "Adult.vs.Immature" "AdultFemale.vs.Ad
 ol.Female" "Adult.Male.vs.SubAd.male"
 $ attacker_sex   : Factor w/ 3 levels "", "F", "M": 3 3 2 2 2 3 2 3 2 2 ..
.
 $ attacker_age   : Factor w/ 2 levels "A","I": 2 2 2 1 1 2 2 1 1 1 ...
 $ N_bites       : num 0 2 1 0 0 0 1 0 0 0 ...
 $ N_drag        : num 0 0 0 0 0 0 0 0 0 0 ...
 $ N_pull        : int 0 0 0 0 0 0 0 0 0 0 ...
 $ N_hit         : num 0 0 0 0 0 0 0 0 0 0 ...
 $ N_caggression : num 0 2 1 0 0 0 1 0 0 0 ...
 $ seconds_visible : Factor w/ 107 levels "1,172","1,407",...: 34 103 94 86
 8 72 64 39 22 22 ...
 $ minutes_visible : num 31.312 13.674 10.931 0.914 1.75 ...
 $ cag_rate      : num NA 0.1463 0.0915 NA NA ...
 $ N_caggression2 : int 0 2 1 0 0 0 1 0 0 0 ...
 $ N_N_pull      : num 0 0 0 0 0 0 0 0 0 0 ...
> data[109,]#This is the atypical point of Emping (the ad)
      attack attacker_group victim_sex_age victims_sex victim_grou
p Victim_ID AttackerID attacker_sex_age attacker_sex
116 20151218PB1_FUNK      PB1      F      F      UN
K      FUNK1      EA      AF      F
      attacker_age N_bites N_drag N_pull N_hit N_caggression seconds_visible
minutes_visible cag_rate N_caggression2 N_N_pull
116      I      30      1      2      0      33      719
      11.97817 2.755013      NA      2
> data[112,]
      attack attacker_group victim_sex_age victims_sex victim_grou
p Victim_ID AttackerID attacker_sex_age attacker_sex
120 20151218PB1_FUNK      PB1      F      F      UN
K      FUNK1      SC      J      M
      attacker_age N_bites N_drag N_pull N_hit N_caggression seconds_visible
minutes_visible cag_rate N_caggression2 N_N_pull
120      I      29      5      0      0      34      1,172
      19.53527 1.740442      NA      0
> data2<-data.frame(data)
> str(data2)
'data.frame': 113 obs. of 20 variables:
 $ attack      : Factor w/ 8 levels "20151218PB1_FUNK",...: 2 2 2 3 8 2
 2 2 4 5 ...

```

```

$ attacker_group : Factor w/ 2 levels "PB1","R1": 2 2 2 2 2 2 2 2 2 2 ..
.
$ victim_sex_age : Factor w/ 5 levels "AF","F","I","J",...: 5 5 5 2 2 5 5
5 2 3 ...
$ victims_sex : Factor w/ 2 levels "F","UNK": 1 1 1 1 1 1 1 1 1 1 ...
$ victim_group : Factor w/ 3 levels "PB1","R2","UNK": 2 2 2 3 1 2 2 2
1 1 ...
$ Victim_ID : Factor w/ 8 levels "EA","Eai","FUNK1",...: 7 7 7 4 8 7
7 7 1 2 ...
$ AttackerID : Factor w/ 48 levels "AF1","AF2","AK",...: 24 47 1 4 4
28 2 40 4 4 ...
$ attacker_sex_age: Factor w/ 5 levels "AF","F","J","M",...: 5 5 1 2 2 5 1
4 2 2 ...
..- attr(*, "contrasts")= num [1:5, 1:4] 1.5 1.5 -1 -1 -1 -1 1.5 -1 1.5
-1 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : chr "AF" "F" "J" "M" ...
.. .. ..$ : chr "Female.vs.Male" "Adult.vs.Immature" "AdultFemale.vs.Ad
ol.Female" "Adult.Male.vs.SubAd.male"
$ attacker_sex : Factor w/ 3 levels "", "F", "M": 3 3 2 2 2 3 2 3 2 2 ..
.
$ attacker_age : Factor w/ 2 levels "A","I": 2 2 2 1 1 2 2 1 1 1 ...
$ N_bites : num 0 2 1 0 0 0 1 0 0 0 ...
$ N_drag : num 0 0 0 0 0 0 0 0 0 0 ...
$ N_pull : int 0 0 0 0 0 0 0 0 0 0 ...
$ N_hit : num 0 0 0 0 0 0 0 0 0 0 ...
$ N_caggression : num 0 2 1 0 0 0 1 0 0 0 ...
$ seconds_visible : Factor w/ 107 levels "1,172","1,407",...: 34 103 94 86
8 72 64 39 22 22 ...
$ minutes_visible : num 31.312 13.674 10.931 0.914 1.75 ...
$ cag_rate : num NA 0.1463 0.0915 NA NA ...
$ N_caggression2 : int 0 2 1 0 0 0 1 0 0 0 ...
$ N_N_pull : num 0 0 0 0 0 0 0 0 0 0 ...
> data2<-data2[-c(109,112),]
> str(data2)
'data.frame': 111 obs. of 20 variables:
$ attack : Factor w/ 8 levels "20151218PB1_FUNK",...: 2 2 2 3 8 2
2 2 4 5 ...
$ attacker_group : Factor w/ 2 levels "PB1","R1": 2 2 2 2 2 2 2 2 2 2 ..
.
$ victim_sex_age : Factor w/ 5 levels "AF","F","I","J",...: 5 5 5 2 2 5 5
5 2 3 ...
$ victims_sex : Factor w/ 2 levels "F","UNK": 1 1 1 1 1 1 1 1 1 1 ...
$ victim_group : Factor w/ 3 levels "PB1","R2","UNK": 2 2 2 3 1 2 2 2
1 1 ...
$ Victim_ID : Factor w/ 8 levels "EA","Eai","FUNK1",...: 7 7 7 4 8 7
7 7 1 2 ...
$ AttackerID : Factor w/ 48 levels "AF1","AF2","AK",...: 24 47 1 4 4
28 2 40 4 4 ...
$ attacker_sex_age: Factor w/ 5 levels "AF","F","J","M",...: 5 5 1 2 2 5 1
4 2 2 ...
..- attr(*, "contrasts")= num [1:5, 1:4] 1.5 1.5 -1 -1 -1 -1 1.5 -1 1.5
-1 ...
.. ..- attr(*, "dimnames")=List of 2
.. .. ..$ : chr "AF" "F" "J" "M" ...
.. .. ..$ : chr "Female.vs.Male" "Adult.vs.Immature" "AdultFemale.vs.Ad
ol.Female" "Adult.Male.vs.SubAd.male"
$ attacker_sex : Factor w/ 3 levels "", "F", "M": 3 3 2 2 2 3 2 3 2 2 ..
.
$ attacker_age : Factor w/ 2 levels "A","I": 2 2 2 1 1 2 2 1 1 1 ...

```

```

$ N_bites      : num  0 2 1 0 0 0 1 0 0 0 ...
$ N_drag       : num  0 0 0 0 0 0 0 0 0 0 ...
$ N_pull       : int   0 0 0 0 0 0 0 0 0 0 ...
$ N_hit        : num  0 0 0 0 0 0 0 0 0 0 ...
$ N_caggression : num  0 2 1 0 0 0 1 0 0 0 ...
$ seconds_visible : Factor w/ 107 levels "1,172","1,407",...: 34 103 94 86
8 72 64 39 22 22 ...
$ minutes_visible : num  31.312 13.674 10.931 0.914 1.75 ...
$ cag_rate       : num  NA 0.1463 0.0915 NA NA ...
$ N_caggression2 : int   0 2 1 0 0 0 1 0 0 0 ...
$ N_N_pull      : num  0 0 0 0 0 0 0 0 0 0 ...
> table(data$attacker_sex_age)#with EA and SC in the IGE 18Dec2015

AF  F  J  M SA
18 58  3 12 22
> table(data2$attacker_sex_age)#without EA and SC in the IGE 18Dec2015

AF  F  J  M SA
17 58  2 12 22
>
>
> contrasts(data2$attacker_sex_age)
      Female.vs.Male Adult.vs.Immature AdultFemale.vs.Adol.Female Adult.Male.
vs.SubAd.male
AF           1.5           -1.0           -1
      0
F           1.5           1.5           1
      0
J          -1.0          -1.0           0
      0
M          -1.0           1.5           0
      1
SA          -1.0          -1.0           0
      -1
>
>
> mod2<-glmer(N_caggression~attacker_sex_age+offset(log(minutes_visible))+
(1|attack/AttackerID), family="poisson", data=data2)
Warning message:
In checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
> summary(mod2)
Generalized linear mixed model fit by maximum likelihood (Laplace Approxim
ation) ['glmerMod']
Family: poisson ( log )
Formula: N_caggression ~ attacker_sex_age + offset(log(minutes_visible)) +
(1 | attack/AttackerID)
Data: data2

      AIC      BIC    logLik deviance df.resid
    221.8    240.7   -103.9    207.8     104

Scaled residuals:
      Min       1Q   Median       3Q      Max
-0.88272 -0.37531 -0.16928 -0.00007  3.11638

Random effects:
Groups              Name      Variance Std.Dev.
AttackerID:attack (Intercept) 1.8283   1.3521

```



```

    attack      (Intercept) 0.9239    0.9612
Number of obs: 111, groups:  AttackerID:attack, 110; attack, 8

Fixed effects:
                                Estimate Std. Error z value Pr(>|z|)
(Intercept)                    -4.826     110.423  -0.044
0.965
attacker_sex_ageFemale.vs.Male    3.293     110.421   0.030
0.976
attacker_sex_ageAdult.vs.Immature -7.666     220.842  -0.035
0.972
attacker_sex_ageAdultFemale.vs.Adol.Female  8.947     276.052   0.032
0.974
attacker_sex_ageAdult.Male.vs.SubAd.male    1.538       1.409   1.091
0.275

Correlation of Fixed Effects:
              (Intr) a__F.. a__A.. a__AF.
attck__F..M -1.000
attck__A..I  1.000 -1.000
at__AF..A.F -1.000  1.000 -1.000
a__A.M..SA.  0.005 -0.003 -0.002  0.002
convergence code: 0
Model is nearly unidentifiable: large eigenvalue ratio
- Rescale variables?
> #The significant difference between adult males and sub-adult males disappear (which I don't get because those data haven't been touched...)
>
>
>
>
> #####GRAPHS#####
>
> #Graphical representation of contact aggression rates
> ggplot(data, aes(x=attacker_sex_age,y=cag_rate))+
+   geom_boxplot()+
+   labs(x="Sex-age class of attackers", y="No.contact aggression per minute")
Warning message:
Removed 81 rows containing non-finite values (stat_boxplot).
>
>
> bystanders<-data[data$N_caggression=="0",]
> table(bystanders$attacker_sex_age)

AF  F  J  M  SA
7 48  1 12 13
>
>
> #Graphical representation of minutes visible (bystanders only)
>
> ggplot(bystanders, aes(x=attacker_sex_age,y=minutes_visible))+
+   geom_boxplot()+
+   labs(x="Sex-age class of bystanders", y="Minutes visible")

```


CHAPTER 5: SUPPLEMENTARY INFORMATION

5.1. Does substituting between-group difference in the number of females by the difference in group size increase the best fit model for the variable “winner” from chapter 3? R Script with results

```
## download packages
install.packages("lme4")#Package that allows to calculate the glms
install.packages("car")#Package to check regression "quality"
install.packages("ggplot2")# To plot independent variables and glms
install.packages("modEvA")# To calculate pseudo R-square in GLMs ( to see to what extend dyads alone account
for the variation)
install.packages("languageR")#To Represent GLMMs with the function plotLMER.fnc
install.packages("ppcor")#To check for correlations between independent variables
install.packages("AICcmodavg")# To use aictab, which constructs model selection tables (Mazerolle 2017)
install.packages("MuMIn")# To calculate R2 with the r.squaredGLMM function
install.packages("sjPlot")# To produce GLMM graphs with CIs and showing the data points
install.packages("dplyr")# Needs to be reinstalled to sjPlot works fine

library(lme4)
library(car)
library(ggplot2)
library(modEvA)
library(languageR)
library(ppcor)
library(AICcmodavg)
library(MuMIn)
library(dplyr)
library(sjPlot)

#Set directory
setwd("C:/Users/Laura/Dropbox/PhD/THESIS/Research Chapters/IGE Group level/Data_Analysis")
getwd()

## Upload data
factors_original<-read.csv("factors_originalv1.csv")

#### Flip the variables for pb1-r1 so R1 is the focal group in all the encounters with decided outcome

#Checking the original data
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
```

```
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]

#Flipping pb1-r1 to r1-pb1
factors_original$winner_analysis[ factors_original$dyad=="pb1r1"] <-1-
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_groupsize[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_groupsize[
factors_original$dyad=="pb1r1"]
factors_original$rel_nummales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_nummales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numfemales[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numfemales[
factors_original$dyad=="pb1r1"]
factors_original$rel_numinfperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfperfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numinfpermale[
factors_original$dyad=="pb1r1"]
factors_original$rel_numswfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_numswfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swgs[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swgs[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfemperfem[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfemperfem[
factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_swfempermale[
factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[ factors_original$dyad=="pb1r1"] <- -factors_original$rel_sexratio[
factors_original$dyad=="pb1r1"]
factors_original$rel_UD190[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_UD190[factors_original$dyad=="pb1r1"]
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"] <- -
factors_original$rel_distancetocorearea[factors_original$dyad=="pb1r1"]

#Checking that the flipping worked
factors_original$winner_analysis[factors_original$dyad=="pb1r1"]
factors_original$rel_numinfpermale[ factors_original$dyad=="pb1r1"]
factors_original$rel_swfempermale[factors_original$dyad=="pb1r1"]
factors_original$rel_sexratio[factors_original$dyad=="pb1r1"]

####Convert variables to the appropriate format
factors_original$num_obs<- as.numeric(factors_original$num_obs)
factors_original$dyad<- factor(factors_original$dyad)
factors_original$winner_analysis<- as.numeric(factors_original$winner_analysis)#If written as factor at this
stage, the flipping goes wrong
factors_original$durationIGE<- as.numeric(factors_original$durationIGE)
factors_original$rel_numfemales<- as.numeric(factors_original$rel_numfemales)
factors_original$rel_nummales<- as.numeric(factors_original$rel_nummales)
factors_original$rel_numinfperfem<- as.numeric(factors_original$rel_numinfperfem)
factors_original$rel_numinfpermale<- as.numeric(factors_original$rel_numinfpermale)
factors_original$rel_numswfem<- as.numeric(factors_original$rel_numswfem)
factors_original$rel_swgs<- as.numeric(factors_original$rel_swgs)
factors_original$rel_swfemperfem<- as.numeric(factors_original$rel_swfemperfem)
factors_original$rel_swfempermale<- as.numeric(factors_original$rel_swfempermale)
factors_original$rel_sexratio<- as.numeric(factors_original$rel_sexratio)
factors_original$rel_UD190<- as.numeric(factors_original$rel_UD190)
factors_original$rel_distancetocorearea<- as.numeric(factors_original$rel_distancetocorearea)
```

```
factors_original$winner_analysis<- as.factor(factors_original$winner_analysis)#Now we can transform it into
factor without problems
```

```
#Eliminating NAs (otherwise when calculating the null models the sample size is different and the comparison
cannot be made)
```

```
missingrows = is.na(factors_original$rel_nummales)
factors_original = factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numfemales)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numinfperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_numinfpermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_swfemperfem)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_swfempermale)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$rel_sexratio)
factors_original= factors_original[!missingrows,]
missingrows = is.na(factors_original$winner_analysis)
factors_original= factors_original[!missingrows,]
```

```
> #####what if we kept the payoff proxies of the female model but use
group size as RHP proxy?
>
> #Null model
> res.null=glmer(winner_analysis ~ 1+ (1|dyad), family="binomial", da
ta=factors_original)
>
> #AIC values to the list
> models<-list()
> models[[1]]<-res.null
> Modnames <- "null model"
>
> #Calculating Marginal and Conditional R2 (According to Nakagawa and
Schielzeth, 2013)
> r2_null<-r.squaredGLMM(res.null)
The result is correct only if all data used by the model has not chang
ed since model was fitted.
> R2<-r2_null
```

```
> #Original model
>
> res_ori=glmer(winner_analysis ~ rel_numfemales+rel_UD190+rel_swfempe
rfem+rel_sexratio+
+ (1|dyad), family="binomial", data=factors_original)
>
>
> print(summary(res_ori))
Generalized linear mixed model fit by maximum likelihood (Laplace Appr
oximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_numfemales + rel_UD190 + rel_swfempe
rfe
m + rel_sexratio + (1 | dyad)
Data: factors_original
```

```

      AIC      BIC    logLik deviance df.resid
124.5    139.7    -56.2    112.5      88

Scaled residuals:
      Min       1Q   Median       3Q      Max
-1.78397 -0.85273  0.05227  0.82087  2.56823

Random effects:
  Groups Name      Variance Std.Dev.
dyad    (Intercept) 0         0
Number of obs: 94, groups: dyad, 2

Fixed effects:
              Estimate Std. Error z value Pr(>|z|)
(Intercept)   -5.952409   2.112424  -2.818  0.00484 **
rel_numfemales  0.505729   0.189859   2.664  0.00773 **
rel_UD190       0.017199   0.006523   2.637  0.00838 **
rel_swfemperfem -5.237037   2.721852  -1.924  0.05435 .
rel_sexratio   -1.189945   0.446535  -2.665  0.00770 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:
              (Intr) r1_nmf r_UD19 r1_swf
rel_numfmls  -0.901
rel_UD190    -0.346  0.367
r1_swfmpfrm  0.096 -0.195 -0.276
rel_sexrati  0.769 -0.476 -0.278  0.268
>
>
> #AIC values to the list
> models[[2]]<-res_ori
> Modnames <-  rbind(Modnames, "Original model (No.fem)")
>
> #Calculating Marginal and Conditional R2
> r2_ori<-r.squaredGLMM(res_ori)
The result is correct only if all data used by the model has not changed since model was fitted.
> R2<-rbind(R2,r2_ori)
> #Model replacing No.females by the group size
>
> res_mix=glmer(winner_analysis ~ rel_groupsize+rel_UD190+rel_swfemperfem+rel_sexratio+
+              (1|dyad), family="binomial", data=factors_original)
>
>
> print(summary(res_mix))
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
Family: binomial ( logit )
Formula: winner_analysis ~ rel_groupsize + rel_UD190 + rel_swfemperfem +
+       rel_sexratio + (1 | dyad)
Data: factors_original

      AIC      BIC    logLik deviance df.resid
127.1    142.4    -57.6    115.1      88

Scaled residuals:
      Min       1Q   Median       3Q      Max
-2.05595 -0.89568  0.08394  0.84340  2.15902

```

Random effects:

Groups Name	Variance	Std.Dev.
dyad (Intercept)	2.459e-17	4.959e-09

Number of obs: 94, groups: dyad, 2

Fixed effects:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-5.461442	2.226391	-2.453	0.0142 *
rel_groupsize	0.311388	0.139148	2.238	0.0252 *
rel_UD190	0.015960	0.006325	2.523	0.0116 *
rel_swfemperfem	-5.184262	2.656126	-1.952	0.0510 .
rel_sexrati	-0.755273	0.389728	-1.938	0.0526 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Correlation of Fixed Effects:

	(Intr)	rl_grp	r_UD19	rl_swf
rel_groupsz	-0.914			
rel_UD190	-0.317	0.325		
rl_swfmpfrm	0.093	-0.187	-0.259	
rel_sexrati	0.475	-0.125	-0.166	0.208

>

> #AIC values to the list

> models[[3]]<-res_mix

> Modnames <- rbind(Modnames, "Group size model")

>

> #Calculating Marginal and Conditional R2

> r2_mix<-r.squaredGLMM(res_mix)

The result is correct only if all data used by the model has not changed since model was fitted.

> R2<-rbind(R2,r2_mix)

>

>

>

> cat("\n\n\n Comparison of mixed model (group size+chapter 3 payoffs) to null model\n\n")

Comparison of mixed model (group size+chapter 3 payoffs) to null mode

1

> print(anova(res.null,res_mix, test="Chisq"))

Data: factors_original

Models:

res.null: winner_analysis ~ 1 + (1 | dyad)

res_mix: winner_analysis ~ rel_groupsize + rel_UD190 + rel_swfemperfem

+

res_mix: rel_sexrati + (1 | dyad)

	Df	AIC	BIC	logLik	deviance	Chisq	Chi	Df	Pr(>Chisq)
res.null	2	130.19	135.27	-63.093	126.19				
res_mix	6	127.13	142.39	-57.566	115.13	11.053		4	0.02597 *

res.null 2 130.19 135.27 -63.093 126.19

res_mix 6 127.13 142.39 -57.566 115.13 11.053 4 0.02597 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

> #The full model wasn't significant (but almost) so no adj. model is produced

> cat("\n\n\n RESULTS \n\n\n")

RESULTS

```
> aictab(cand.set=models, modnames = Modnames, second.ord = TRUE, nobs  
= NULL, sort = TRUE)
```

Model selection based on AICc:

	K	AICc	Delta_AICc	AICcWt	Cum.Wt	LL
Original model (No.fem)	6	125.43	0.00	0.74	0.74	-56.23
Group size model	6	128.10	2.67	0.20	0.94	-57.57
null model	2	130.32	4.88	0.06	1.00	-63.09

```
> R2
```

	R2m	R2c
R2	0.0000000	0.09929656
r2_ori	0.2536879	0.25368793
r2_mix	0.2120426	0.21204264

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